

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:31:34 ; Search time 523.667 Seconds
(without alignments)
1500.527 Million cell updates/sec

Title: US-09-821-734-12
Perfect score: 27
Sequence: 1 ctcttcacgaaccgactcggtgtg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		GenEmbl:
1:	gb_ba:	*
2:	gb_htg:	*
3:	gb_in:	*
4:	gb_om:	*
5:	gb_ov:	*
6:	gb_ph:	*
7:	gb_pl:	*
8:	gb_pr:	*
9:	gb_ro:	*
10:	gb_sts:	*
11:	gb_sy:	*
12:	gb_un:	*
13:	gb_vi:	*
14:	em_ba:	*
15:	em_fun:	*
16:	em_hum:	*
17:	em_in:	*
18:	em_mu:	*
19:	em_om:	*
20:	em_or:	*
21:	em_ov:	*
22:	em_pat:	*
23:	em_ph:	*
24:	em_pl:	*
25:	em_ro:	*
26:	em_sts:	*
27:	em_un:	*
28:	em_vi:	*
29:	em_htg_hum:	*
30:	em_htg_inv:	*
31:	em_htg_other:	*
32:	em_htg_mus:	*
33:	em_htg_pln:	*
34:	em_htg_rod:	*
35:	em_htg_mam:	*
36:	em_htg_vrt:	*
37:	em_sy:	*
38:	em_htgo_hum:	*
39:	em_htgo_mus:	*
40:	em_htgo_other:	*
41:		

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	27	100.0	27	6	AX268374	AX268374 Sequence
2	27	100.0	127	11	AF008934	AF008934 Homo sapi
3	27	100.0	129	9	HSU93599	U93599 Homo sapien
4	27	100.0	444	11	G53000	G53000 SHGC-81785
5	27	100.0	1641	9	AF107214	AF107214 Homo sapi
6	27	100.0	2253	6	AX467227	AX467227 Sequence
7	27	100.0	2253	9	AY101595	AY101595 Homo sapi
8	27	100.0	2472	9	BC025672	BC025672 Homo sapi
9	27	100.0	2518	9	AF176574	AF176574 Homo sapi
10	27	100.0	2558	6	AX376036	AX376036 Sequence
11	27	100.0	2653	6	AX337498	AX337498 Sequence
12	27	100.0	2653	6	I23794	I23794 Sequence 1
13	27	100.0	2653	9	HUMPSM	M99487 Human prost
14	27	100.0	93525	9	AF007544	AF007544 Homo sapi
15	27	100.0	117521	2	AC023784	AC023784 Homo sapi
16	27	100.0	129095	9	AC110742	AC110742 Homo sapi
17	27	100.0	158524	2	AL162372	AL162372 Homo sapi
C 18	27	100.0	187638	2	AC118273	AC118273 Homo sapi
19	23	85.2	198	9	AF016826	AF016826 Homo sapi
C 20	20.6	76.3	199052	2	AC122962	AC122962 Rattus no
21	20.2	74.8	246865	2	AC074003	AC074003 Homo sapi
22	19.8	73.3	2532	4	AF050502	AF050502 Sus scrof
23	19.2	71.1	119451	2	AF003958	AF003958 Oryza sat
24	19.2	71.1	125687	2	AP004743	AP004743 Oryza sat
C 25	19.2	71.1	332635	1	AP003005	AP003005 Mesorhizo
26	19	70.4	51920	2	CER08A5	Z82281 Caenorhabdi
C 27	19	70.4	130027	9	AC004982	AC004982 Homo sapi
28	19	70.4	133402	9	AL137843	AL137843 Human DNA
29	18.6	68.9	64920	1	AE008925	AE008925 Xanthomon
C 30	18.6	68.9	93294	9	AL607144	AL607144 Human DNA
31	18.6	68.9	142762	2	AL391599	AL391599 Homo sapi
C 32	18.6	68.9	161456	2	AC078869	AC078869 Homo sapi
C 33	18.6	68.9	171968	2	AC125965	AC125965 Rattus no
34	18.6	68.9	184480	2	AC016887	AC016887 Homo sapi
C 35	18.6	68.9	214793	2	AC023345	AC023345 Homo sapi
36	18.6	68.9	216599	2	AC087379	AC087379 Homo sapi
37	18.6	68.9	306050	1	RME603645	AL603645 Rhizobium
38	18.4	68.1	1071	5	AF168111	AF168111 Playa mel
C 39	18.4	68.1	349980	6	AX344571	AX344571 Sequence
C 40	18.4	68.1	349980	6	AX344572	AX344572 Sequence
41	18.2	67.4	9704	2	AC017694	AC017694 Drosophil
42	18.2	67.4	19750	3	AE002980	AE002980 Drosophil
43	18.2	67.4	204167	2	AC110553	AC110553 Mus muscu
C 44	18	66.7	208	9	HSLN2C55	U66787 Human lamin
45	18	66.7	424	9	HSA323185	AJ323185 Homo sapi

ALIGNMENTS

RESULT 1	AX268374	AX268374	27 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	Sequence 12 from Patent WO0174845.					
DEFINITION	AX268374					
ACCESSION	AX268374.1	GI:16541581				
VERSION						
KEYWORDS	synthetic construct.					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1					
AUTHORS	Pedyczak,A., Chong,P. and Sia,C.D.					
TITLE	Immunogenic peptides derived from prostate-specific membrane antigen (psma) and uses thereof					
JOURNAL	Patent: WO 0174845-A 12 11-OCT-2001;					

FEATURES
source
Aventis Pasteur Limited (CA)
Location/Qualifiers
1. .27
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="CLP326"
BASE COUNT 5 a 10 c 6 g 6 t
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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
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Db 1 CTCCTTCACGAAACCGACTCGGCTGTG 27

RESULT 2
AF008934
LOCUS
DEFINITION Homo sapiens prostate-specific membrane antigen related sequence,
sequence tagged site.
ACCESSION AF008934
VERSION AF008934.1 GI:2393914
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Maraj,B.H., Whelan,P. and Markham,A.F.
TITLE Prostate-Specific Membrane Antigen Related Gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 127)
AUTHORS Maraj,B.H., Whelan,P. and Markham,A.F.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1997) Molecular Medicine Unit, Leeds University,
Beckett, Leeds, Yorkshire LS9 7TF, England

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1. .127
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q14"
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/clone_lib="NIGMS coriell panel for chromosome 11
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BASE COUNT 12 a 40 c 42 g 33 t
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
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Db 10 CTCCTTCACGAAACCGACTCGGCTGTG 36

RESULT 3
HSU93599
LOCUS
DEFINITION Homo sapiens PSM pseudogene, partial sequence.
ACCESSION U93599
VERSION U93599.1 GI:1928993
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 129)

AUTHORS Maraj,B.H., Leek,J.P., Karayi,M., Ali,M., Lench,N.J. and Markham,A.F.
TITLE Detailed genetic mapping around a putative prostate-specific membrane antigen locus on human chromosome 11p11.2
JOURNAL Cytoenet. Cell Genet. 81 (1), 3-9 (1998)
MEDLINE 98358137
PUBMED 9691167
REFERENCE 2 (bases 1 to 129)
AUTHORS Maraj,B.H., Bailey,A., Carr,I.M. and Markham,A.F.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-1997) Molecular Medicine Unit, Leeds University,
Beckett Street, Leeds, West Yorkshire LS9 7TF, England

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/map="11q14"
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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
|||||
Db 10 CTCCTTCACGAAACCGACTCGGCTGTG 36

RESULT 4
G53000
LOCUS
DEFINITION SHGC-81785 Human Homo sapiens STS genomic, linear STS 30-MAR-2000
ACCESSION G53000
VERSION G53000.1 GI:5224177
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT
Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: ACGGAGGCATTAGTGAGATTGAG
Primer B: AGAGGAAGCCGAGGAGAAAGAA
STS size: 230
PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Amplifaq Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 Seconds
(without alignments)
614.181 Million cell updates/sec

Title: US-09-821-734-12
Perfect score: 27
Sequence: 1 ctccttcacgaaccgactcggtgtg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	22 AAS15139	Human DNA encoding
2	27	100.0	101	21 AAF16465	Human prostate can
3	27	100.0	866	21 AAF15696	Human prostate can
4	27	100.0	2253	21 AAA09454	Human prostate spe
5	27	100.0	2558	21 AAC78599	Human PRO739 nucle
6	27	100.0	2558	22 AAS45976	Human DNA encoding
7	27	100.0	2653	15 AAQ65520	Prostate-specific
8	27	100.0	2653	24 ABK86204	CDNA encoding huma
9	27	100.0	2653	24 ABK64556	Human benign prost

10	27	100.0	2653	24	ABL69670	Prostate cancer re
11	27	100.0	2654	17	AAT36785	Prostate-specific
12	27	100.0	2884	23	ABV22873	Human prostate exp
13	27	100.0	2884	23	ABV23013	Human prostate exp
14	27	100.0	2884	23	ABV28703	Human prostate exp
15	27	100.0	2884	23	ABV28849	Human prostate exp
16	27	100.0	3017	17	AAT36776	Prostate-specific
17	27	100.0	3017	17	AAT36786	Prostate-specific
C 18	23	85.2	24	22	AAD17629	Human FGCP gene sp
C 19	18	66.7	98	22	ABA51445	Human breast cell
C 20	18	66.7	98	22	ABA69473	Human foetal liver
C 21	18	66.7	98	22	ABA36398	Probe #14864 for g
C 22	18	66.7	98	22	AAK17728	Human brain expres
C 23	18	66.7	98	22	AAK43549	Human bone marrow
C 24	18	66.7	98	22	AAI24335	Probe #14268 for g
C 25	18	66.7	98	22	AAI49605	Probe #18291 used
C 26	18	66.7	98	22	AAI09877	Probe #9868 used t
C 27	18	66.7	98	24	ABSI7686	Human genome-deriv
28	18	66.7	339	20	AAV90178	EST clone DF780.
29	18	66.7	339	20	AAV89499	EST clone COL187.
C 30	18	66.7	470	22	ABA46343	Human breast cell
C 31	18	66.7	470	22	ABA56908	Human foetal liver
C 32	18	66.7	470	22	ABA26523	Probe #4989 for ge
C 33	18	66.7	470	22	AAK05005	Human brain expres
C 34	18	66.7	470	22	AAK30539	Human bone marrow
C 35	18	66.7	470	22	AAI15155	Probe #5088 for ge
C 36	18	66.7	470	22	AAI36483	Probe #5169 used t
C 37	18	66.7	470	22	AAI04898	Probe #4889 used t
C 38	18	66.7	470	24	ABS05182	Human genome-deriv
C 39	18	66.7	3554	12	AAQ13225	Merotin gene. Hom
C 40	18	66.7	3554	16	AAQ86479	Merotin partial cD
41	18	66.7	4408	24	ABL61776	Colon adenocarcino
C 42	18	66.7	4598	24	ABK35727	CDNA sequence #118
C 43	18	66.7	9419	21	AAK88894	Human laminin 2 al
C 44	18	66.7	9420	21	AAK88892	Human laminin 2 al
C 45	18	66.7	9534	16	AAT17419	Merotin cDNA. Hom

ALIGNMENTS

RESULT 1
AAS15139
ID AAS15139 standard; DNA; 27 BP.
XX
AC AAS15139;
XX
DT 16-JAN-2002 (first entry)
XX
DE Human DNA encoding a PSMA derived immunogenic peptide CLP326.
XX
KW Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;
KW tumour; immunogenic peptide; cytostatic; gene therapy; CLP326.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..27
FT /*tag= a
FT /product= "CLP326"
FT /partial
FT /note= "No start or stop codon"

XX	WO200174845-A2.
PN	
XX	11-OCT-2001.
PD	
XX	
PF	30-MAR-2001; 2001WO-CA00411.
XX	
PR	31-MAR-2000; 2000US-193386P.
XX	
PA	(AVET) AVENTIS PASTEUR LTD.
XX	

PI Pedyczak A, Chong P, Sia CDY;
XX WPI; 2001-626378/72.
DR P-PSDB; AAU09104.
XX
PT New polypeptides useful for inducing an immune response and treating
PT prostate cancer comprises polypeptides derived from the prostate
PT specific membrane antigen.
XX
PS Claim 6; Page 15; 47pp; English.
XX
CC The invention relates to prostate specific membrane antigen (PSMA)
CC derived peptides (and the nucleic acids encoding them) capable of
CC eliciting an immune response. The molecules of the invention are used to
CC elicit an immune response, particularly to treat cancer and tumours,
CC especially prostate cancer. Delivery of the peptides may be by
CC expression from the nucleic acids encoding them (i.e. gene therapy).
CC The present sequence encodes a PSMA derived immunogenic peptide.
XX
SQ Sequence 27 BP; 5 A; 10 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
Db 1 CTCCTTCACGAAACCGACTCGGCTGTG 27

RESULT 2
AAFL16465
ID AAF16465 standard; cDNA; 101 BP.
XX
AC AAF16465;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:900.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR P-PSDB; AAB57262.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer.
XX
PS Claim 1; Page 1341; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF15506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 101 BP; 16 A; 34 C; 32 G; 14 T; 5 other;

Query Match 100.0%; Score 27; DB 21; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
Db 61 CTCCTTCACGAAACCGACTCGGCTGTG 87

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ID AAF15696 standard; cDNA; 866 BP.
XX
AC AAF15696;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:131.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR P-PSDB; AAB56493.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer.
XX
PS Claim 1; Page 697-698; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds
(without alignments)
394.299 Million cell updates/sec

Title: US-09-821-734-12
Perfect score: 27
Sequence: 1 ctccttcacgaacccgactcggctgtg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	27	100.0	2653	1 US-08-325-553-1	Sequence 1, Appli
2	27	100.0	2653	2 US-08-394-152A-1	Sequence 1, Appli
C 3	27	100.0	2957	2 US-08-394-152A-48	Sequence 48, Appl
4	27	100.0	3017	2 US-08-394-152A-39	Sequence 39, Appl
C 5	18	66.7	3554	2 US-08-460-309-1	Sequence 1, Appli
C 6	18	66.7	3554	2 US-08-125-077-1	Sequence 1, Appli
C 7	18	66.7	3554	6 5444158-1	Patent No. 5444158
8	17.4	64.4	4657	3 US-09-254-325-1	Sequence 1, Appli
9	17.4	64.4	5643	3 US-09-079-415-5	Sequence 5, Appli
10	17.4	64.4	5643	3 US-08-750-458A-1	Sequence 1, Appli
C 11	17.2	63.7	606	4 US-08-998-416-106	Sequence 106, App
C 12	17.2	63.7	718	4 US-08-998-416-611	Sequence 611, App
C 13	17.2	63.7	1809	1 US-08-204-196A-3	Sequence 3, Appli
C 14	17.2	63.7	1809	1 US-08-204-196A-4	Sequence 4, Appli
15	17	63.0	286	3 US-08-688-988-12	Sequence 12, Appl
C 16	17	63.0	628	1 US-08-686-878A-1	Sequence 1, Appli
C 17	17	63.0	1893	1 US-08-271-667B-5	Sequence 5, Appli
C 18	17	63.0	1893	3 US-08-765-889C-18	Sequence 18, Appl
C 19	17	63.0	1893	5 PCT-US95-07855-18	Sequence 18, Appl
C 20	17	63.0	2101	3 US-08-765-889C-5	Sequence 5, Appli
C 21	17	63.0	2101	5 PCT-US95-07855-5	Sequence 5, Appli
C 22	17	63.0	2166	4 US-09-175-928-1	Sequence 5, Appli
C 23	17	63.0	2304	1 US-08-271-667B-6	Sequence 6, Appli
C 24	17	63.0	2304	3 US-08-765-889C-19	Sequence 19, Appl
C 25	17	63.0	2304	5 PCT-US95-07855-19	Sequence 19, Appl
C 26	17	63.0	2430	2 US-08-820-170A-35	Sequence 35, Appl
C 27	17	63.0	2430	3 US-09-055-699-35	Sequence 35, Appl

C 28	17	63.0	2430	4 US-09-273-565-35	Sequence 35, Appl
C 29	17	63.0	2430	4 US-09-565-538-35	Sequence 35, Appl
C 30	17	63.0	2430	4 US-09-661-468-35	Sequence 35, Appl
C 31	17	63.0	2977	2 US-08-020-170A-36	Sequence 36, Appl
C 32	17	63.0	2977	3 US-09-055-699-36	Sequence 36, Appl
C 33	17	63.0	2977	4 US-09-273-565-36	Sequence 36, Appl
C 34	17	63.0	2977	4 US-09-565-538-36	Sequence 36, Appl
C 35	17	63.0	2977	4 US-09-661-468-36	Sequence 36, Appl
36	16.4	60.7	1454	2 US-08-657-392-1	Sequence 1, Appli
37	16.4	60.7	1454	5 PCT-US94-02539-1	Sequence 1, Appli
38	16.4	60.7	1455	2 US-08-657-392-26	Sequence 26, Appl
39	16.4	60.7	1455	5 PCT-US94-02539-26	Sequence 26, Appl
40	16	59.3	614	4 US-09-385-982-399	Sequence 399, App
C 41	16	59.3	660	4 US-08-981-030-4	Sequence 4, Appli
C 42	16	59.3	1596	1 US-08-513-841-3	Sequence 3, Appli
C 43	16	59.3	1596	2 US-08-696-834-3	Sequence 3, Appli
C 44	16	59.3	1596	2 US-08-942-673-3	Sequence 3, Appli
C 45	16	59.3	1596	4 US-09-118-317-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-325-553-1
; Sequence 1, Application US/08325553
; Patent No. 5538866
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,553
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,337A
; FILING DATE: 05 NOV 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/41426
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Carcinoma
; IMMEDIATE SOURCE:

;; CLONE: Prostate-Specific Membrane Antigen
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 262..2511
US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
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Db 271 CTCCTTCACGAAACCGACTCGGCTGTG 297

RESULT 2
US-08-394-152A-1
; Sequence 1, Application US/08394152A
; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israel, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen

FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 271 CTCCTTCACGAAACCGACTCGGCTGTG 297
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RESULT 3
US-08-394-152A-48/C
; Sequence 48, Application US/08394152A
; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israel, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2957 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen

US-08-394-152A-48
Query Match 100.0%; Score 27; DB 2; Length 2957;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
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Db 263 CTCCTTCACGAAACCGACTCGGCTGTG 237

RESULT 4
US-08-394-152A-39
; Sequence 39, Application US/08394152A
; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israel, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds
(without alignments)
703.471 Million cell updates/sec

Title: US-09-821-734-12
Perfect score: 27
Sequence: 1 CTCCTTCACGAACCGACTCGGCTGTG 27

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Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues
Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	27	100.0	101	10	US-09-925-300-900
3	27	100.0	866	10	US-09-925-300-131
4	27	100.0	2558	9	US-09-978-295A-617
5	27	100.0	2558	9	US-09-978-697-617
6	27	100.0	2558	9	US-09-978-192A-617
7	27	100.0	2558	9	US-09-999-832A-617
8	27	100.0	2558	9	US-09-978-189-617
9	27	100.0	2558	9	US-10-174-590-103
10	27	100.0	2558	9	US-10-176-758-103
11	27	100.0	2558	9	US-10-175-737-103
12	27	100.0	2558	9	US-10-173-706-103
13	27	100.0	2558	9	US-10-175-738-103
14	27	100.0	2558	9	US-10-175-752-103
15	27	100.0	2558	9	US-10-176-482-103
16	27	100.0	2558	9	US-10-176-757-103
17	27	100.0	2558	9	US-10-176-913-103
18	27	100.0	2558	9	US-10-180-552-103
19	27	100.0	2558	9	US-10-180-557-103

20	27	100.0	2558	9	US-10-173-700-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
24	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
27	27	100.0	2558	9	US-10-175-743-103	Sequence 103, App
28	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
29	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
36	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
37	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
40	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
42	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
43	27	100.0	2558	9	US-10-174-586-103	Sequence 103, App
44	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-09-821-734-12
; Sequence 12, Application US/09821734
; Publication No. US20030027246A1
; GENERAL INFORMATION:
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Artur
; APPLICANT: Sia, Charles Dwo Yuan
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane
; TITLE OF INVENTION: (PSMA) and Uses Thereof
; FILE REFERENCE: 11014-22
; CURRENT APPLICATION NUMBER: US/09/821,734
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,386
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CLP326
US-09-821-734-12

Query Match 100.0%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTCACGAACCGACTCGGCTGTG 27
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Db 1 CTCCTTCACGAACCGACTCGGCTGTG 27

RESULT 2
US-09-925-300-900
; Sequence 900, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 900
LENGTH: 101
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (29)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (40)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (54)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (89)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (99)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-900

Query Match 100.0%; Score 27; DB 10; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27
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Db 61 CTCCTTCACGAAACCGACTCGGCTGTG 87

RESULT 3
US-09-925-300-131
Sequence 131, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
LENGTH: 866
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (683)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (723)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (740)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (793)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (813)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (841)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-131

Query Match 100.0%; Score 27; DB 10; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 220 CTCCTTCACGAAACCGACTCGGCTGTG 246

RESULT 4
US-09-978-295A-617
Sequence 617, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PLC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:33:49 ; Search time 828.5 seconds
(without alignments)
527.795 Million cell updates/sec

Title: US-09-821-734-12
Perfect score: 27
Sequence: 1 ctccttcacgaacccgactcggctgtg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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	12:	gb_est3:	*				
	13:	gb_est4:	*				
	14:	gb_est5:	*				
	15:	em_estfun:	*				
	16:	em_estom:	*				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	405	10 AV692993	AV692993 AV692993
2	27	100.0	420	10 AW898913	AW898913 CM0-NN007
3	27	100.0	444	17 AQ053523	AQ053523 RPCI11-50
4	27	100.0	484	17 AQ636441	AQ636441 RPCI-11-4
5	27	100.0	704	13 BI772735	BI772735 603053273
6	27	100.0	882	14 BQ708386	BQ708386 AGENCOURT

7	27	100.0	902	14 BQ708480	BQ708480 AGENCOURT
8	27	100.0	904	14 BQ893679	BQ893679 AGENCOURT
9	27	100.0	914	14 BQ712611	BQ712611 AGENCOURT
10	27	100.0	917	14 BQ711571	BQ711571 AGENCOURT
11	27	100.0	937	14 BQ894290	BQ894290 AGENCOURT
12	27	100.0	939	14 BQ712351	BQ712351 AGENCOURT
13	27	100.0	998	14 BQ711650	BQ711650 AGENCOURT
14	27	100.0	1187	14 BM926125	BM926125 AGENCOURT
15	26	96.3	949	9 AL563971	AL563971 AL563971
16	21.4	79.3	200	14 N79392	N79392 yz74a08.r1
17	20.2	74.8	539	13 BJ040403	BJ040403 BJ040403
18	20.2	74.8	578	13 BJ065301	BJ065301 BJ065301
19	19	70.4	320	14 H79070	H79070 yu24h02.r1
20	19	70.4	543	14 BQ143427	BQ143427 fhm1c.pk0
21	18.8	69.6	649	17 AG140363	AG140363 Pan trogl
22	18.6	68.9	334	14 W82655	W82655 mf06e10.r1
23	18.6	68.9	474	10 BB807530	BB807530 BB807530
24	18.6	68.9	507	9 AA530080	AA530080 vj37b01.r
25	18.6	68.9	515	9 AA261631	AA261631 mz87c12.r
26	18.6	68.9	579	10 BB241564	BB241564 BB241564
27	18.6	68.9	683	14 BQ444546	BQ444546 UI-M-ER0-
28	18.6	68.9	788	12 BG069703	BG069703 H3079B12-
29	18.6	68.9	1289	12 BF670658	BF670658 602149893
30	18.6	68.9	1701	11 AK008165	AK008165 Mus muscu
31	18.6	68.9	2043	11 BC016206	BC016206 Mus muscu
32	18.6	68.9	2077	11 BC025124	BC025124 Mus muscu
33	18.2	67.4	409	14 R67855	R67855 yi28d11.s1
34	18.2	67.4	879	14 BQ429613	BQ429613 AGENCOURT
35	18	66.7	278	10 BB331421	BB331421 BB331421
36	18	66.7	290	10 BB099715	BB099715 BB099715
37	18	66.7	311	10 BB260750	BB260750 BB260750
38	18	66.7	361	9 AI739100	AI739100 wi18a01.x
39	18	66.7	424	14 T37532	T37532 EST102680 S
40	18	66.7	447	10 BB670080	BB670080 BB670080
41	18	66.7	448	14 W00091	W00091 TgESTzy75e0
42	18	66.7	449	10 BB732533	BB732533 BB732533
43	18	66.7	450	10 BB670068	BB670068 BB670068
44	18	66.7	463	10 AW297115	AW297115 UI-H-BI2-
45	18	66.7	510	10 BE663548	BE663548 147407 MA

ALIGNMENTS

RESULT 1	AV692993	AV692993	405 bp	mRNA	linear	EST 16-JAN-2002
LOCUS	AV692993	GKC Homo sapiens	CDNA clone	GKCCDB09 5'	mRNA sequence.	
DEFINITION	AV692993	EST				
ACCESSION	AV692993.1	GI:10294856				
VERSION	AV692993.1	EST				
KEYWORDS	human.					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 405)					
AUTHORS	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.					
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	98	(26),	15089-15094	(2001)	
MEDLINE	21625106					
COMMENT	Contact: Zeguangu Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.					

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:31:34 ; Search time 523.667 Seconds
(without alignments)
1500.527 Million cell updates/sec

Title: US-09-821-734-13
Perfect score: 27
Sequence: 1 gtgctggcgggtggcttcttctcctc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :					GenEmbl:				
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					2:	gb_htg:	*		
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					4:	gb_om:	*		
					5:	gb_ov:	*		
					6:	gb_pat:	*		
					7:	gb_ph:	*		
					8:	gb_pl:	*		
					9:	gb_pr:	*		
					10:	gb_ro:	*		
					11:	gb_sts:	*		
					12:	gb_sy:	*		
					13:	gb_un:	*		
					14:	gb_vi:	*		
					15:	em_ba:	*		
					16:	em_fun:	*		
					17:	em_hum:	*		
					18:	em_in:	*		
					19:	em_mu:	*		
					20:	em_om:	*		
					21:	em_or:	*		
					22:	em_ov:	*		
					23:	em_pat:	*		
					24:	em_ph:	*		
					25:	em_pl:	*		
					26:	em_ro:	*		
					27:	em_sts:	*		
					28:	em_un:	*		
					29:	em_vi:	*		
					30:	em_htg_hum:	*		
					31:	em_htg_inv:	*		
					32:	em_htg_other:	*		
					33:	em_htg_mus:	*		
					34:	em_htg_pln:	*		
					35:	em_htg_rod:	*		
					36:	em_htg_mam:	*		
					37:	em_htg_vrt:	*		
					38:	em_sy:	*		
					39:	em_htgo_hum:	*		
					40:	em_htgo_mus:	*		
					41:	em_htgo_other:	*		

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	27	100.0	27	6	AX268375	Sequence
2	27	100.0	72	6	AR077260	Sequence
3	27	100.0	127	11	AF008934	Homo sapi
4	27	100.0	129	9	HS093599	Homo sapien
5	27	100.0	198	9	AF016826	Homo sapi
6	27	100.0	444	11	G53000	SHGC-81785
7	27	100.0	1641	9	AF107214	Homo sapi
8	27	100.0	2253	6	AX467227	Sequence
9	27	100.0	2253	9	AY101595	Homo sapi
10	27	100.0	2472	9	BC025672	Homo sapi
11	27	100.0	2518	9	AF176574	Homo sapi
12	27	100.0	2558	6	AX376036	Sequence
13	27	100.0	2653	6	AX337498	Sequence
14	27	100.0	2653	6	I23794	Sequence 1
15	27	100.0	2653	9	HUMPSM	Human prost
16	27	100.0	93525	9	AF007544	Homo sapi
17	27	100.0	117521	2	AC023784	Homo sapi
18	27	100.0	129095	9	AC110742	Homo sapi
19	27	100.0	158524	2	AL162372	Homo sapi
20	27	100.0	187638	2	AC118273	Homo sapi
21	25.4	94.1	246865	2	AC074003	Homo sapi
22	23	85.2	592	9	HSA7318	Homo sapi
23	20.6	76.3	103656	10	AL713958	Mouse DNA
24	20.6	76.3	237588	2	AC025581	Mus muscu
25	20.2	74.8	134725	2	AC109418	Rattus no
26	20.2	74.8	151453	2	AC118988	Sus scrof
27	20.2	74.8	173168	2	AC114035	Rattus no
28	20.2	74.8	202748	10	MMU307670	Mus muscu
29	20.2	74.8	217073	2	AC094162	Rattus no
30	20.2	74.8	237181	2	AC126441	Mus muscu
31	19.8	73.3	171787	2	AC126967	Rattus no
32	19.8	73.3	240422	2	AL805929	Mus muscu
33	19.6	72.6	462	6	AX438611	Sequence
34	19.6	72.6	11546	1	AE002032	Deinococc
35	19.6	72.6	96276	9	HSJ117516	Human DNA
36	19.6	72.6	111117	2	AC097920	Rattus no
37	19.6	72.6	121786	2	AC127998	Rattus no
38	19.6	72.6	157192	2	AP005395	Oryza sat
39	19.6	72.6	161012	2	AP004277	Oryza sat
40	19.6	72.6	169833	2	AC107249	Rattus no
41	19.6	72.6	177562	9	HS269M15	Human DNA
42	19.6	72.6	180865	2	AP003766	Oryza sat
43	19.6	72.6	200218	2	AC117248	Mus muscu
44	19.6	72.6	321519	2	AL714004	Homo sapi
45	19.4	71.9	110000	2	LMFLCHR26_1	Continuation (2 of

ALIGNMENTS

RESULT 1	AX268375	AX268375	Sequence 13 from Patent WO0174845.	27 bp	DNA	linear i	PAT 29-OCT-2001
LOCUS	AX268375	AX268375	AX268375	27 bp	DNA		
DEFINITION	AX268375	AX268375	AX268375	27 bp	DNA		
ACCESSION	AX268375	AX268375	AX268375	27 bp	DNA		
VERSION	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		
KEYWORDS	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		
SOURCE	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		
ORGANISM	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		
REFERENCE	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		
AUTHORS	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		
TITLE	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		
JOURNAL	AX268375.1	AX268375.1	AX268375.1	27 bp	DNA		

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OM nucleic - nucleic search, using sw model.

Run on: April 14, 2003, 09:27:29 ; Search time 99 Seconds
(without alignments)
614.181 Million cell updates/sec

Title: US-09-821-734-13
Perfect score: 27
Sequence: 1 gtgctggcgggtggcttcttctctc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	22	AAS15140 Human DNA encoding
2	27	100.0	72	18	AAT89210 Prostate specific
3	27	100.0	866	21	AAF15696 Human prostate can
4	27	100.0	2253	21	AAA09454 Human prostate spe
5	27	100.0	2558	21	AAC78599 Human PRO739 nucle
6	27	100.0	2558	22	AAS45976 Human DNA encoding
7	27	100.0	2653	15	AAQ65520 Prostate-specific
8	27	100.0	2653	24	ABK86204 cDNA encoding huma
9	27	100.0	2653	24	ABK64556 Human benign prost

10	27	100.0	2653	24	ABL69670	Prostate cancer re
11	27	100.0	2654	17	AAT36785	Prostate-specific
12	27	100.0	2884	23	ABV22873	Human prostate exp
13	27	100.0	2884	23	ABV23013	Human prostate exp
14	27	100.0	2884	23	ABV28703	Human prostate exp
15	27	100.0	2884	23	ABV28849	Human prostate exp
16	27	100.0	3017	17	AAT36776	Prostate-specific
17	27	100.0	3017	17	AAT36786	Prostate-specific
18	21.2	78.5	687	24	ABQ91413	M. capsulatus gene
c 19	19.6	72.6	462	24	ABK79735	Bacillus clausii g
20	19	70.4	5090	19	AAV53575	Nucleotide sequenc
c 21	18.6	68.9	2500	23	ABL16703	Drosophila melanog
22	18.6	68.9	3261	23	AAS89027	DNA encoding novel
23	18.6	68.9	12216	23	ABL16702	Drosophila melanog
24	18.2	67.4	713	23	ABL13269	Drosophila melanog
25	18.2	67.4	3144	23	ABL13268	Drosophila melanog
26	18.2	67.4	3914	23	ABL12804	Drosophila melanog
c 27	18	66.7	459	19	AAV31291	E. coli J96 pathog
28	18	66.7	678	24	ABT03011	Human breast speci
29	18	66.7	1388	21	AAC49992	Arabidopsis thalia
30	18	66.7	1390	21	AAC36747	Arabidopsis thalia
c 31	18	66.7	1470	17	AAT30650	P. gingivalis haem
c 32	18	66.7	1470	19	AAV58871	Haemagglutinin pro
c 33	18	66.7	1841	17	AAT30651	P. gingivalis haem
c 34	18	66.7	1841	19	AAV58872	Haemagglutinin pro
35	18	66.7	1872	21	AAA05527	Streptococcus pneu
36	18	66.7	3472	23	AAS72696	DNA encoding novel
37	18	66.7	10004	22	ABA14483	Human nervous syst
38	18	66.7	10246	22	ABA14485	Human nervous syst
39	18	66.7	10254	19	AAV52162	Streptococcus pneu
c 40	18	66.7	10732	21	AAA10594	Gene encoding a su
c 41	17.8	65.9	2297	21	AAZ93309	Sequence encoding
c 42	17.6	65.2	148	21	AAC24222	Human secreted pro
c 43	17.6	65.2	175	21	AAC12195	Human secreted pro
44	17.6	65.2	240	21	AAC12713	Human secreted pro
c 45	17.6	65.2	265	22	AAI80499	Human polynucleoti

ALIGNMENTS

RESULT 1

AAS15140
ID AAS15140 standard; DNA; 27 BP.

XX AAS15140;

XX 16-JAN-2002 (first entry)

XX Human DNA encoding a PSMA derived immunogenic peptide CLP328.

KW Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;
KW tumour; immunogenic peptide; cytostatic; gene therapy; CLP328.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 1..27

FT /*tag= a

FT /product= "CLP328"

FT /partial

FT /note= "No start or stop codon"

XX WO200174845-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-CA00411.

XX 31-MAR-2000; 2000US-193386P.

XX (AVET) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sia CDY;
XX
DR WPI; 2001-626378/72.
XX P-PSDB; AAU09105.
PT New polypeptides useful for inducing an immune response and treating
PT prostate cancer comprises polypeptides derived from the prostate
PT specific membrane antigen -
XX
PS Claim 6; Page 15; 47pp; English.
XX
CC The invention relates to prostate specific membrane antigen (PSMA)
CC derived peptides (and the nucleic acids encoding them) capable of
CC eliciting an immune response. The molecules of the invention are used to
CC elicit an immune response, particularly to treat cancer and tumours,
CC especially prostate cancer. Delivery of the peptides may be by
CC expression from the nucleic acids encoding them (i.e. gene therapy).
CC The present sequence encodes a PSMA derived immunogenic peptide.
XX
SQ Sequence 27 BP; 0 A; 8 C; 9 G; 10 T; 0 other;

Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
Db 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27

RESULT 2
AAT89210
ID AAT89210 standard; DNA; 72 BP.
XX
AC AAT89210;
XX
DT 30-APR-1998 (first entry)
XX
DE Prostate specific membrane antigen mRNA probe 1.
XX
KW Prostate specific membrane antigen; PSMA; probe; hybridisation;
KW cancer; vaccine; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9738313-A1.
XX
PD 16-OCT-1997.
XX
PF 02-APR-1997; 97WO-US05586.
XX
PR 05-APR-1996; 96US-0014929.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Lesko SA, Nelson WG, Partin AW, Tso POP, Wang Z;
XX
DR WPI; 1997-512878/47.
XX
PT Isolating rare cells by density gradient separation then negative
PT selection - used for enriching prostatic cancer cells for diagnosis,
PT staging and monitoring of disease
XX
PS Claim 12; Page 21; 63pp; English.
XX
CC This sequence is a probe for prostate specific membrane antigen (PSMA),
CC particularly useful for in situ hybridisation. The probe is used to
CC detect the epithelial cells of prostatic cancer cells, via the
CC detection of PSA (prostate specific antigen) and/or PSMA. The method
CC is especially used to enrich prostatic cancer cells from blood,
CC allowing detection and characterisation of these cells for diagnosis,
CC staging and monitoring of disease. It can also be applied to the

CC enrichment of liver, hepatoma, hepatocarcinoma or cancer cells in
CC general.
XX
SQ Sequence 72 BP; 2 A; 18 C; 27 G; 25 T; 0 other;

Query Match 100.0%; Score 27; DB 18; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
Db 22 GTGCTGGCGGGTGGCTTCTTTCTCCTC 48

RESULT 3
AAF15696
ID AAF15696 standard; cDNA; 866 BP.
XX
AC AAF15696;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:131.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR P-PSDB; AAB56493.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
PS Claim 1; Page 697-698; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 866 BP; 236 A; 193 C; 213 G; 215 T; 9 other;

Query Match 100.0%; Score 27; DB 21; Length 866;

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds
(without alignments)
394.299 Million cell updates/sec

Title: US-09-821-734-13
Perfect score: 27
Sequence: 1 gtgctggcgggtggtcttcttctctc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	DB ID	Description
1	27	100.0	72	2 US-08-832-468-1	Sequence 1, Appli
2	27	100.0	2653	1 US-08-325-553-1	Sequence 1, Appli
3	27	100.0	2653	2 US-08-394-152A-1	Sequence 1, Appli
c 4	27	100.0	2957	2 US-08-394-152A-48	Sequence 48, Appl
5	27	100.0	3017	2 US-08-394-152A-39	Sequence 39, Appl
c 6	18	66.7	459	4 US-08-976-259-105	Sequence 105, App
c 7	18	66.7	1265	4 US-09-221-017B-566	Sequence 566, App
c 8	18	66.7	1470	1 US-08-570-311-3	Sequence 3, Appli
c 9	18	66.7	1470	2 US-08-353-485-3	Sequence 3, Appli
c 10	18	66.7	1841	1 US-08-570-311-5	Sequence 5, Appli
c 11	18	66.7	1841	2 US-08-353-485-5	Sequence 5, Appli
12	18	66.7	10254	4 US-08-961-527-29	Sequence 29, Appl
13	17.4	64.4	522	2 US-08-768-964-14	Sequence 14, Appl
c 14	17.4	64.4	522	2 US-08-768-964-15	Sequence 15, Appl
15	17.4	64.4	522	3 US-09-005-299-14	Sequence 15, Appl
c 16	17.4	64.4	522	3 US-09-005-299-15	Sequence 15, Appl
17	17.4	64.4	522	4 US-09-515-431-14	Sequence 14, Appl
c 18	17.4	64.4	522	4 US-09-515-431-15	Sequence 15, Appl
19	17.4	64.4	590	1 US-08-580-038-15	Sequence 15, Appl
20	17.4	64.4	591	1 US-08-580-038-5	Sequence 5, Appli
21	17.4	64.4	591	1 US-08-580-038-12	Sequence 12, Appl
22	17.4	64.4	592	1 US-08-580-038-19	Sequence 19, Appl
23	17.4	64.4	597	2 US-08-768-964-11	Sequence 11, Appl
c 24	17.4	64.4	597	2 US-08-768-964-16	Sequence 16, Appl
25	17.4	64.4	597	3 US-09-005-299-11	Sequence 11, Appl
c 26	17.4	64.4	597	3 US-09-005-299-16	Sequence 16, Appl
27	17.4	64.4	597	4 US-09-515-431-11	Sequence 11, Appl

c 28	17.4	64.4	597	4 US-09-515-431-16	Sequence 16, Appl
29	17.4	64.4	633	1 US-08-580-038-84	Sequence 84, Appl
c 30	17.4	64.4	714	2 US-08-768-964-6	Sequence 6, Appli
31	17.4	64.4	714	2 US-08-768-964-8	Sequence 8, Appli
c 32	17.4	64.4	714	3 US-09-005-299-6	Sequence 6, Appli
c 33	17.4	64.4	714	3 US-09-005-299-8	Sequence 8, Appli
34	17.4	64.4	714	4 US-09-515-431-6	Sequence 6, Appli
c 35	17.4	64.4	714	4 US-09-515-431-8	Sequence 8, Appli
36	17.4	64.4	789	2 US-08-768-964-4	Sequence 4, Appli
c 37	17.4	64.4	789	2 US-08-768-964-5	Sequence 5, Appli
38	17.4	64.4	789	3 US-09-005-299-4	Sequence 4, Appli
c 39	17.4	64.4	789	3 US-09-005-299-5	Sequence 5, Appli
40	17.4	64.4	789	4 US-09-515-431-4	Sequence 4, Appli
c 41	17.4	64.4	789	4 US-09-515-431-5	Sequence 5, Appli
42	17.4	64.4	1069	2 US-08-768-964-1	Sequence 1, Appli
c 43	17.4	64.4	1069	2 US-08-768-964-3	Sequence 3, Appli
44	17.4	64.4	1069	3 US-09-005-299-1	Sequence 1, Appli
c 45	17.4	64.4	1069	3 US-09-005-299-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-832-468-1
; Sequence 1, Application US/08832468
; Patent No. 5962237
; GENERAL INFORMATION:
; APPLICANT: Ts'o, Paul O.P.
; APPLICANT: Wang, Zheng-Pin
; APPLICANT: Lesko, Stephen A.
; APPLICANT: Nelson, William G.
; APPLICANT: Partin, Alan W.
; TITLE OF INVENTION: A METHOD OF ENRICHING RARE CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: 700 Thirteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,468
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60-014929
; FILING DATE: 05-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Jeremy M.
; REGISTRATION NUMBER: 33587
; REFERENCE/DOCKET NUMBER: 72466
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-737-6770
; TELEFAX: 202-737-6776
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
; US-08-832-468-1

Query Match 100.0%; Score 27; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.0047;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
|||||
Db 22 GTGCTGGCGGGTGGCTTCTTTCTCCTC 48

RESULT 2

US-08-325-553-1
; Sequence 1, Application US/08325553
; Patent No. 5538866
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,553
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,337A
; FILING DATE: 05 NOV 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/41426
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Carcinoma
; IMMEDIATE SOURCE:
; CLONE: Prostate-Specific Membrane Antigen
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 262..2511

US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
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Db 340 GTGCTGGCGGGTGGCTTCTTTCTCCTC 366

RESULT 3

US-08-325-553-1

US-08-394-152A-1
; Sequence 1, Application US/08394152A
; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM 330 466 DX2
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,152A
; FILING DATE: 24-FEB-95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41426-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Carcinoma
; IMMEDIATE SOURCE:
; CLONE: Prostate-Specific Membrane Antigen
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 262..2511

US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
|||||
Db 340 GTGCTGGCGGGTGGCTTCTTTCTCCTC 366

RESULT 4

US-08-394-152A-48/C
; Sequence 48, Application US/08394152A
; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds
(without alignments)
703.471 Million cell updates/sec

Title: US-09-821-734-13
Perfect score: 27
Sequence: 1 gtgctggcgggtgcttcttctctc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	866	10 US-09-925-300-131
3	27	100.0	2558	9 US-09-978-295A-617
4	27	100.0	2558	9 US-09-978-697-617
5	27	100.0	2558	9 US-09-978-192A-617
6	27	100.0	2558	9 US-09-999-832A-617
7	27	100.0	2558	9 US-09-978-189-617
8	27	100.0	2558	9 US-10-174-590-103
9	27	100.0	2558	9 US-10-176-758-103
10	27	100.0	2558	9 US-10-175-737-103
11	27	100.0	2558	9 US-10-173-706-103
12	27	100.0	2558	9 US-10-175-738-103
13	27	100.0	2558	9 US-10-175-752-103
14	27	100.0	2558	9 US-10-176-482-103
15	27	100.0	2558	9 US-10-176-757-103
16	27	100.0	2558	9 US-10-176-913-103
17	27	100.0	2558	9 US-10-180-552-103
18	27	100.0	2558	9 US-10-180-557-103
19	27	100.0	2558	9 US-10-173-700-103

20	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
24	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-743-103	Sequence 103, App
27	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
28	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
29	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
36	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
37	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
40	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
42	27	100.0	2558	9	US-10-174-586-103	Sequence 103, App
43	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
44	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-485-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-09-821-734-13
; Sequence 13, Application US/09821734
; Publication NO. US20030027246A1
; GENERAL INFORMATION:
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Artur
; APPLICANT: Sia, Charles Dwo Yuan
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane
; TITLE OF INVENTION: (PSMA) and Uses Thereof
; FILE REFERENCE: 11014-22
; CURRENT APPLICATION NUMBER: US/09/821,734
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,386
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CLP328
US-09-821-734-13

Query Match 100.0%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGGGGTGCTTCTTTCTCCTC 27
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Db 1 GTGCTGGGGGTGCTTCTTTCTCCTC 27

RESULT 2
US-09-925-300-131
; Sequence 131, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAL01
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
LENGTH: 866
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (683)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (723)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (740)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (793)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (813)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (841)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-131

Query Match 100.0%; Score 27; DB 10; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTCTCCTC 27
|||||
Db 289 GTGCTGGCGGGTGGCTTCTTCTCCTC 315

RESULT 3
US-09-978-295A-617
Sequence 617, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:33:49 ; Search time 828.5 Seconds
(without alignments)
527.795 Million cell updates/sec

Title: US-09-821-734-13
Perfect score: 27
Sequence: 1 gtgctgcggttggtgctttcttcctc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	405	10 AV692993	AV692993 AV692993
2	27	100.0	420	10 AW898913	AW898913 CM0-NN007
3	27	100.0	444	17 AQ053523	AQ053523 RPC111-50
4	27	100.0	484	17 AQ636441	AQ636441 RPC11-11-4
5	27	100.0	704	13 BI772735	BI772735 603053273
6	27	100.0	882	14 BQ708386	BQ708386 AGENCOURT

7	27	100.0	902	14 BQ708480	BQ708480 AGENCOURT
8	27	100.0	904	14 BQ893679	BQ893679 AGENCOURT
9	27	100.0	914	14 BQ712611	BQ712611 AGENCOURT
10	27	100.0	917	14 BQ711571	BQ711571 AGENCOURT
11	27	100.0	937	14 BQ894290	BQ894290 AGENCOURT
12	27	100.0	939	14 BQ712351	BQ712351 AGENCOURT
13	27	100.0	949	9 AL563971	AL563971 AL563971
14	27	100.0	998	14 BQ711650	BQ711650 AGENCOURT
15	27	100.0	1187	14 BM926125	BM926125 AGENCOURT
c 16	22.2	82.2	993	14 BQ944302	BQ944302 AGENCOURT
c 17	20.6	76.3	448	17 AZ773575	AZ773575 2M0001N06
c 18	20.6	76.3	489	17 AZ463400	AZ463400 1M0272007
c 19	20.6	76.3	496	9 AI047158	AI047158 uh62a06.r
c 20	20.6	76.3	502	12 BE864299	BE864299 UI-M-BH1-
c 21	20.6	76.3	749	14 BQ572291	BQ572291 UI-M-FD0-
c 22	20.6	76.3	773	9 AU035488	AU035488 AU035488
c 23	20.6	76.3	782	9 AI069211	AI069211 mgae0005d
c 24	20.6	76.3	804	12 BF531575	BF531575 602091233
c 25	20.2	74.8	923	17 CNS022R0	AL178533 Tetraodon
c 26	20.2	74.8	1101	14 BQ137346	BQ137346 NF065B12S
c 27	19.8	73.3	1049	12 BG026698	BG026698 602293545
c 28	19.6	72.6	350	14 W45099	W45099 zc20q11.r1
c 29	19.6	72.6	392	14 R86318	R86318 yo62b09.r1
c 30	19.6	72.6	474	17 AQ556075	AQ556075 HS_2079_A
c 31	19.6	72.6	509	14 H08966	H08966 y196a05.r1
c 32	19.6	72.6	824	17 AG135962	AG135962 Pan trogl
c 33	19.6	72.6	1101	17 CNS05FDY	AL334879 Tetraodon
c 34	19.4	71.9	606	10 BE414920	BE414920 MML006.G0
c 35	19.2	71.1	419	12 BE770361	BE770361 PM0-FT005
c 36	19.2	71.1	446	14 BQ091832	BQ091832 UMN22C08
c 37	19.2	71.1	568	17 AZ644005	AZ644005 1M0507G17
c 38	19.2	71.1	729	17 AQ746914	AQ746914 HS_2275_A
c 39	19.2	71.1	934	14 BQ924251	BQ924251 AGENCOURT
c 40	19	70.4	131	17 AZ463519	AZ463519 1M0272I21
c 41	19	70.4	192	10 AW380321	AW380321 QV3-HT026
c 42	19	70.4	210	14 H86284	H86284 yt04d12.r1
c 43	19	70.4	214	14 R84925	R84925 yt65c03.r1
c 44	19	70.4	220	10 BE481508	BE481508 166982 BA
c 45	19	70.4	282	9 AA019516	AA019516 ze57g01.r

ALIGNMENTS

RESULT 1
AV692993
LOCUS AV692993 405 bp mRNA linear EST 16-JAN-2002
DEFINITION AV692993 GKC Homo sapiens cDNA clone GKCDDB09 5', mRNA sequence.
ACCESSION AV692993
VERSION AV692993.1 GI:10294856
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES source Location/Qualifiers 1. .405 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="GKCCDB09" /clone_lib="GKC" /tissue_type="hepatocellular carcinoma" /dev_stage="Adult" /lab_host="SOLR" /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI" 85 a 107 c 121 g 91 t 1 others

BASE COUNT 85 a 107 c 121 g 91 t 1 others

ORIGIN

Query Match 100.0%; Score 27; DB 10; Length 405; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
|||||

Db 232 GTGCTGGCGGGTGGCTTCTTTCTCCTC 258

RESULT 2

AW898913

LOCUS AW898913 420 bp mRNA linear EST 24-MAY-2000

DEFINITION CM0-NN0079-140400-334-f10 NN0079 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW898913

VERSION AW898913.1 GI:8063118

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 420)

REFERENCE 1 (bases 1 to 420)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM0-NN0079-140400-334-f10&t3=2000-04-14&t4=1) Seq primer: puc 18 forward High quality sequence stop: 420.

FEATURES source Location/Qualifiers 1. .420 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="NN0079" /dev_stage="Adult" /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 118 a 100 c 89 g 113 t

ORIGIN

Query Match 100.0%; Score 27; DB 10; Length 420; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
|||||

Db 82 GTGCTGGCGGGTGGCTTCTTTCTCCTC 108

RESULT 3

AQ053523

LOCUS AQ053523 444 bp DNA linear GSS 20-APR-1999

DEFINITION RPC111-50L10.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-50L10, DNA sequence.

ACCESSION AQ053523

VERSION AQ053523.1 GI:3348446

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 444)

REFERENCE 1 (bases 1 to 444)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)

JOURNAL Unpublished (1998)

COMMENT Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@ejlong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html Class: BAC ends.

FEATURES source Location/Qualifiers 1. .444 /organism="Homo sapiens" /db_xref="GDB:7519089" /db_xref="taxon:9606" /clone="RPCI-11-50L10" /clone_lib="RPCI-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC Library" 62 a 120 c 173 g 89 t

BASE COUNT 62 a 120 c 173 g 89 t

ORIGIN

Query Match 100.0%; Score 27; DB 17; Length 444; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTTCTCCTC 27
|||||

Db 204 GTGCTGGCGGGTGGCTTCTTTCTCCTC 230

RESULT 4

AQ636441

LOCUS AQ636441 484 bp DNA linear GSS 17-JUN-1999

DEFINITION RPCI-11-477N9.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-477N9, DNA sequence.

ACCESSION AQ636441

VERSION AQ636441.1 GI:5099076

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003; 09:31:34 ; Search time 523.667 Seconds
(without alignments)
1500.527 Million cell updates/sec

Title: US-09-821-734-14
Perfect score: 27
Sequence: 1 gagctagcacattatgatgtcctgttg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	100.0	27	6	AX268376	AX268376 Sequence
2	27	100.0	198	9	AF016828	AF016828 Homo sapi
3	27	100.0	592	9	HSA7318	AJ007318 Homo sapi
4	27	100.0	2253	6	AX467227	AX467227 Sequence
5	27	100.0	2253	9	AY101595	AY101595 Homo sapi
6	27	100.0	2472	9	BC025672	BC025672 Homo sapi
7	27	100.0	2518	9	AF176574	AF176574 Homo sapi
8	27	100.0	2653	6	AX337498	AX337498 Sequence
9	27	100.0	2653	6	I23794	I23794 Sequence 1
10	27	100.0	2653	9	HUMPSM	M99487 Human prost
11	27	100.0	117521	2	AC023784	AC023784 Homo sapi
12	27	100.0	129095	9	AC110742	AC110742 Homo sapi
13	27	100.0	158524	2	AL162372	AL162372 Homo sapi
14	27	100.0	187638	2	AC118273	AC118273 Homo sapi
15	27	100.0	246865	2	AC074003	AC074003 Homo sapi
16	25.4	94.1	2061	6	AX403107	AX403107 Sequence
17	25.4	94.1	2558	6	AX376036	AX376036 Sequence
18	25.4	94.1	93525	9	AF007544	AF007544 Homo sapi
19	25.4	94.1	135637	9	AP003400	AP003400 Homo sapi
20	25.4	94.1	192648	2	AC024234	AC024234 Homo sapi
21	22.2	82.2	2532	4	AF050502	AF050502 Sus scrof
22	20.6	76.3	2259	10	AF513486	AF513486 Rattus no
23	20.6	76.3	2348	10	AF040256	AF040256 Rattus no
24	20.6	76.3	2899	10	RNU75973	U75973 Rattus norv
25	20.6	76.3	234784	2	AC106536	AC106536 Rattus no
26	20.6	76.3	235731	2	AC097423	AC097423 Rattus no
27	19.8	73.3	186191	2	AC126532	AC126532 Rattus no
28	19.6	72.6	653	11	G56278	G56278 SHGC-101792
29	19.6	72.6	2314	3	AY060661	AY060661 Drosophil
30	19.6	72.6	32819	2	AC014478	AC014478 Drosophil
31	19.6	72.6	65558	2	AC116742	AC116742 Mus muscu
32	19.6	72.6	71307	2	AC008296	AC008296 Drosophil
33	19.6	72.6	82600	8	AP005149	AP005149 Oryza sat
34	19.6	72.6	83684	9	AC105290	AC105290 Homo sapi
35	19.6	72.6	83714	2	AC008297	AC008297 Drosophil
36	19.6	72.6	103889	8	ATT24C20	AL096856 Arabidops
37	19.6	72.6	146174	2	AC095369	AC095369 Rattus no
38	19.6	72.6	154066	9	HS24O18	AL021808 Human DNA
39	19.6	72.6	154216	9	AC073071	AC073071 Homo sapi
40	19.6	72.6	164682	9	AC006199	AC006199 Homo sapi
41	19.6	72.6	165080	2	AC117493	AC117493 Homo sapi
42	19.6	72.6	175335	3	AC091636	AC091636 Drosophil
43	19.6	72.6	177607	9	AC090642	AC090642 Homo sapi
44	19.6	72.6	178216	2	AC051662	AC051662 Homo sapi
45	19.6	72.6	190478	2	AC130127	AC130127 Rattus no

ALIGNMENTS

RESULT 1	AX268376	AX268376	Sequence 14 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268376	AX268376	AX268376				
DEFINITION	AX268376	AX268376	AX268376				
ACCESSION	AX268376	AX268376	AX268376				
VERSION	AX268376.1	AX268376.1	GI:16541583				
KEYWORDS	AX268376.1	AX268376.1	GI:16541583				
SOURCE	AX268376	AX268376	AX268376				
ORGANISM	AX268376	AX268376	AX268376				
REFERENCE	AX268376	AX268376	AX268376				
AUTHORS	AX268376	AX268376	AX268376				
TITLE	AX268376	AX268376	AX268376				
JOURNAL	AX268376	AX268376	AX268376				

FEATURES source
Aventis Pasteur Limited (CA)
Location/Qualifiers
1. .27.
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="CLP330"
6 a 5 c 7 g 9 t
BASE COUNT 6 a 5 c 7 g 9 t
ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCTAGCACATTATGATGTCCTGTTG 27
|||||
Db 1 GAGCTAGCACATTATGATGTCCTGTTG 27
RESULT 2
AF016828 198 bp DNA linear PRI 23-JUL-2001
LOCUS Homo sapiens prostate specific-membrane antigen gene, provisional
DEFINITION exon 3.
ACCESSION AF016828
VERSION AF016828.1 GI:2335205
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 198)
AUTHORS Maraj,B.H.; Leek,J.P.; Karayi,M.; Ali,M.; Lench,N.J. and Markham,A.F.
TITLE Detailed genetic mapping around a putative prostate-specific
membrane antigen locus on human chromosome 11p11.2
JOURNAL Cytogenet. Cell Genet. 81 (1), 3-9 (1998)
MEDLINE 98358137
PUBMED 9691167
REFERENCE 2 (bases 1 to 198)
AUTHORS Maraj,B., Whelan,P. and Markham,A.F.
TITLE Prostate specific-membrane antigen gene exon/intron
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 198)
AUTHORS Maraj,B., Whelan,P. and Markham,A.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1997) Molecular Medicine Unit, Leeds University,
Beckett Street, Leeds, West Yorkshire LS9 7TF, England
FEATURES source
Location/Qualifiers
1. .198
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11p11.2"
1. .145
/note="provisional exon 3"
146. .198
/note="provisional intron 3"
71 a 42 c 28 g 57 t
BASE COUNT 71 a 42 c 28 g 57 t
ORIGIN
Query Match 100.0%; Score 27; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCTAGCACATTATGATGTCCTGTTG 27
|||||
Db 59 GAGCTAGCACATTATGATGTCCTGTTG 85
RESULT 3
HSA7318 592 bp mRNA linear PRI 21-JUN-1999
LOCUS Homo sapiens mRNA for prostate-specific membrane antigen, splice
DEFINITION

variant, partial.
AJ007318
AJ007318.1 GI:5139498
alternative splicing; prostate-specific membrane antigen; psm gene.
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Noack,B., Pilarsky,C.P., Schmidt,U., Froehner,M. and Wirth,M.P.
TITLE A new splice variant of prostate-specific membrane antigen
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 592)
AUTHORS Noack,B.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1998) Noack B., Department of Urology, Technical
University of Dresden, Fetscherstr. 74, Dresden 01307, GERMANY
COMMENT Related sequence: AF007544, M99487.
FEATURES source
Location/Qualifiers
1. .592
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="x5"
/sex="male"
/cell_line="LNCap"
/tissue_type="prostatic carcinoma metastatic lymph node"
1. .560
/gene="psm"
<1. .35
/gene="psm"
/number=2
36. .133
/gene="psm"
/note="alternative splicing; exon not present in alternate
psm transcript M99487"
134. .239
/gene="psm"
/number=2
240. .426
/gene="psm"
/number=3
427. .528
/gene="psm"
/number=4
548. .553
/gene="psm"
/note="putative"
560
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/note="putative"
208 a 120 c 107 g 157 t
BASE COUNT 208 a 120 c 107 g 157 t
ORIGIN
Query Match 100.0%; Score 27; DB 9; Length 592;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCTAGCACATTATGATGTCCTGTTG 27
|||||
Db 340 GAGCTAGCACATTATGATGTCCTGTTG 366
RESULT 4
AX467227 2253 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 1 from Patent WO0234287.
DEFINITION
ACCESSION AX467227
VERSION AX467227.1 GI:21900509
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 Seconds
(without alignments)
614.181 Million cell updates/sec

Title: US-09-821-734-14
Perfect score: 27
Sequence: 1 gagctagcacattatgatgtcctgttg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues 4370478
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	100.0	27	AAS15141	Human DNA encoding
2	27	100.0	60	ABN42303	Human spliced tran
3	27	100.0	866	AAF15696	Human prostate can
4	27	100.0	2226	AAA12732	DNA encoding a hum
5	27	100.0	2253	AAA09454	Human prostate spe
6	27	100.0	2653	AAQ65520	Prostate-specific
7	27	100.0	2653	ABK86204	CDNA encoding huma
8	27	100.0	2653	ABK64556	Human benign prost
9	27	100.0	2653	ABL69670	Prostate cancer re

10	27	100.0	2654	17	AAT36785	Prostate-specific
11	27	100.0	2884	23	ABV22873	Human prostate exp
12	27	100.0	2884	23	ABV23013	Human prostate exp
13	27	100.0	2884	23	ABV28703	Human prostate exp
14	27	100.0	2884	23	ABV28849	Human prostate exp
15	25.4	94.1	2061	24	AAD34009	Human gene 4 cDNA
16	25.4	94.1	2558	21	AAC78599	Human PRO739 nucle
17	25.4	94.1	2558	22	AAS45976	Human DNA encoding
18	22.4	83.0	789	17	AAT36779	Prostate-specific
19	22.4	83.0	1280	17	AAT36789	Prostate-specific
20	19.6	72.6	1077	21	AAC50963	Arabidopsis thalia
21	19.6	72.6	3527	23	ABL28852	Drosophila melanog
22	19	70.4	1143	21	AAC79245	Human lung tumour
23	19	70.4	1143	23	AAD23321	Human lung tumour
24	19	70.4	1414	23	AAS79889	DNA encoding novel
25	18.6	68.9	279	23	ABV60526	Human prostate exp
26	18.4	68.1	22	22	AAD17635	Human GCPII gene e
27	18.2	67.4	489	21	AAF11645	Aspergillus niger
28	18	66.7	580	22	ABA59984	Human foetal liver
29	18	66.7	580	22	AAK08255	Human brain expres
30	18	66.7	580	22	AAK34134	Human bone marrow
31	18	66.7	580	22	AAI39857	Probe #8543 used t
32	18	66.7	580	24	ABS08897	Human genome-deriv
33	18	66.7	2449	23	ABL21808	Drosophila melanog
34	18	66.7	2456	23	ABL21846	Drosophila melanog
35	18	66.7	48328	22	AAF28540	Genomic fragment #
36	17.6	65.2	1564	21	AAC33440	Arabidopsis thalia
37	17.6	65.2	2297	20	AAH84085	TCV S1 protein cod
38	17.6	65.2	2297	20	AAH84084	TCV S1 protein cod
39	17.6	65.2	2297	20	AAH84086	TCV S1 protein cod
40	17.6	65.2	2297	20	AAH84091	BCV S1 protein cod
41	17.6	65.2	3738	13	AAQ31412	Bacillus thuringie
42	17.6	65.2	3738	18	AAT66802	Bacillus thuringie
43	17.6	65.2	3738	18	AAT60045	86Q3a toxin coding
44	17.6	65.2	3738	19	AAV58982	B.t. toxin gene 86
45	17.6	65.2	3738	21	AAA65094	Bacillus thuringie

ALIGNMENTS

RESULT 1
AAS15141
ID AAS15141 standard; DNA; 27 BP.
XX
AC AAS15141;
XX
DT 16-JAN-2002 (first entry)
XX
DE Human DNA encoding a PSMA derived immunogenic peptide CLP330.
XX
KW Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;
KW tumour; immunogenic peptide; cytostatic; gene therapy; CLP330.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..27
FT /*tag= a.
FT /product= "CLP330"
FT /partial
FT /note= "No start or stop codon"

WO200174845-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-CA00411.

31-MAR-2000; 2000US-193386P.

(AVET) AVENTIS PASTEUR LTD.


```
PI Pedyczak A, Chong P, Sia CDY;
XX WPI; 2001-626378/72.
DR P-PSDB; AAU09106.
XX
PT New polypeptides useful for inducing an immune response and treating
PT prostate cancer comprises polypeptides derived from the prostate
PT specific membrane antigen -
XX
PS Claim 6; Page 15; 47pp; English.
XX
CC The invention relates to prostate specific membrane antigen (PSMA)
CC derived peptides (and the nucleic acids encoding them) capable of
CC eliciting an immune response. The molecules of the invention are used to
CC elicit an immune response, particularly to treat cancer and tumours,
CC especially prostate cancer. Delivery of the peptides may be by
CC expression from the nucleic acids encoding them (i.e. gene therapy).
CC The present sequence encodes a PSMA derived immunogenic peptide.
XX
SQ Sequence 27 BP; 6 A; 5 C; 7 G; 9 T; 0 other;

Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGTCCTGTTG 27
Db 1 GAGCTAGCACATTATGATGTCCTGTTG 27

RESULT 2
ABN42303
ID ABN42303 standard; DNA; 60 BP.
XX
AC ABN42303;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:15051.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 15051; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of

the genome, which encodes one or more messenger RNA splice variants.
The oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies, in qualitatively or
quantitatively characterising the corresponding transcriptome, and in
detecting RNA transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialised mini
libraries to detect transcripts of a sub-transcriptome under a
particular biological or pathological state, and so allowing the
detection of tissue- and pathology-specific genes such as those genes
only expressed in specific tissue under a specific pathological
condition; to detect developmental specific genes; and to detect RNA
transcripts and splice variants of a transcriptome of a patient suffering
from a particular disorder. ABN27253 to ABN59589 represent
oligonucleotide sequences from rats, humans and mice, which are used in
the exemplification of the present invention.
N.B. The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 17 A; 17 C; 9 G; 17 T; 0 other;

Query Match 100.0%; Score 27; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGTCCTGTTG 27
Db 4 GAGCTAGCACATTATGATGTCCTGTTG 30

RESULT 3
AAF15696
ID AAF15696 standard; CDNA; 866 BP.
XX
AC AAF15696;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:131.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR P-PSDB; AAB56493.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
PS Claim 1; Page 697-698; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds
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394.299 Million cell updates/sec

Title: US-09-821-734-14
Perfect score: 27
Sequence: 1 gagctagcacattatgatgtcctgttg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	27	100.0	2653	1	US-08-325-553-1
3	27	100.0	2653	2	US-08-394-152A-1
4	22.4	83.0	789	2	US-08-394-152A-42
5	19	70.4	1143	4	US-09-370-838-287
6	17.6	65.2	3738	1	US-08-158-232-7
7	17.6	65.2	3738	1	US-08-304-626-7
8	17.6	65.2	3738	1	US-08-611-928-7
9	17.6	65.2	3738	3	US-09-173-891-7
10	17.4	64.4	1194	4	US-09-134-001C-1267
11	17.4	64.4	5519	4	US-09-453-702B-226
12	17	63.0	2457	1	US-08-486-013-68
13	17	63.0	2457	2	US-08-482-279-68
14	17	63.0	2457	2	US-08-342-268-68
15	17	63.0	2457	3	US-09-015-968-68
16	17	63.0	2457	4	US-09-397-386-68
17	17	63.0	90050	4	US-09-245-041-5
18	16.6	61.5	152331	3	US-09-128-155-16
19	16.6	61.5	176373	3	US-09-134-001C-216
20	16.4	60.7	669	4	US-09-134-001C-216
21	16.4	60.7	1066	5	PCT-US92-00282-14
22	16.2	60.0	302	4	US-09-060-756-253
23	16.2	60.0	741	4	US-09-199-637A-406
24	16.2	60.0	3597	4	US-09-199-637A-404
25	16.2	60.0	8075	3	US-08-374-077C-1
26	16.2	60.0	8075	4	US-08-895-590-1
27	16.2	60.0	8075	4	US-09-539-879A-1

28	16.2	60.0	42235	4	US-09-199-637A-1	Sequence 1, Appli
29	16	59.3	1741	4	US-09-232-160-4	Sequence 4, Appli
30	16	59.3	1974	1	US-08-413-135-3	Sequence 3, Appli
31	16	59.3	1974	4	US-08-971-395-3	Sequence 3, Appli
32	16	59.3	3054	4	US-09-484-970B-138	Sequence 138, App
33	16	59.3	44453	4	US-09-146-053-5	Sequence 5, Appli
34	16	59.3	84495	4	US-09-797-906-3	Sequence 3, Appli
35	15.8	58.5	1221	3	US-08-965-600-2	Sequence 2, Appli
36	15.8	58.5	1221	4	US-09-489-506-2	Sequence 2, Appli
37	15.8	58.5	1247	2	US-08-647-960-1	Sequence 1, Appli
38	15.8	58.5	1952	3	US-08-714-918-39	Sequence 39, Appl
39	15.8	58.5	1952	4	US-09-265-315-39	Sequence 39, Appl
40	15.8	58.5	1952	4	US-09-265-315-39	Sequence 39, Appl
41	15.8	58.5	1952	4	US-09-266-417-39	Sequence 39, Appl
42	15.8	58.5	2418	3	US-08-669-286-4	Sequence 4, Appli
43	15.8	58.5	2418	4	US-09-469-253-4	Sequence 4, Appli
44	15.8	58.5	2418	4	US-09-642-146-4	Sequence 4, Appli
45	15.8	58.5	3003	4	US-09-423-340-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-164-034B-1

GENERAL INFORMATION:

APPLICANT: Mincheff, Milcho S.
Loukinov, I. Dmitri
Zoubak, Serguei

TITLE OF INVENTION: Immunotherapy of Cancer Through Expression
of Truncated Tumor- Or Tumor-Associated Antigen

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: William S. Ramsey,

Ramsey, Cook, Looper & Kurlander, LLC
STREET: 10420 Little Patuxent Parkway, Suite 250

CITY: Columbia

STATE: Maryland

COUNTRY: USA

ZIP: 21044

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: PC

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect 8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/164,034B

FILING DATE: 30-Sep-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ramsey, William S.

REGISTRATION NUMBER: 32,715

REFERENCE/DOCKET NUMBER: bril

TELECOMMUNICATION INFORMATION:

TELEPHONE: (410) 992-9660

TELEFAX: (410) 992-9540

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-164-034B-1

Query Match 100.0%; Score 27; DB 4; Length 2133;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGCTCTGTTG 27
|||||
Db 199 GAGCTAGCACATTATGATGCTCTGTTG 225

RESULT 2

US-08-325-553-1

Sequence 1, Application US/08325553

Patent No. 5538866

GENERAL INFORMATION:

APPLICANT: Israeli, Ron S.

APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,553
FILING DATE: 05 NOV 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-325-553-1
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Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 586 GAGCTAGCACATTATGATGTCCTGTTG 612
RESULT 3
US-08-394-152A-1
Sequence 1, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-394-152A-1
Query Match 100.0%; Score 27; DB 2; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 586 GAGCTAGCACATTATGATGTCCTGTTG 612
RESULT 4
US-08-394-152A-42
Sequence 42, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds
(without alignments)
703.471 Million cell updates/sec

Title: US-09-821-734-14
Perfect score: 27
Sequence: 1 gagctagcacattatgatgtcctgttg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	9	US-09-821-734-14
2	27	100.0	866	10	US-09-925-300-131
3	27	100.0	2653	9	US-10-094-699-2
4	27	100.0	2653	10	US-09-969-708-536
5	25.4	94.1	2558	9	US-09-978-295A-617
6	25.4	94.1	2558	9	US-09-978-697-617
7	25.4	94.1	2558	9	US-09-978-192A-617
8	25.4	94.1	2558	9	US-09-999-832A-617
9	25.4	94.1	2558	9	US-09-978-189-617
10	25.4	94.1	2558	9	US-10-174-590-103
11	25.4	94.1	2558	9	US-10-176-758-103
12	25.4	94.1	2558	9	US-10-175-737-103
13	25.4	94.1	2558	9	US-10-173-706-103
14	25.4	94.1	2558	9	US-10-175-738-103
15	25.4	94.1	2558	9	US-10-175-752-103
16	25.4	94.1	2558	9	US-10-176-482-103
17	25.4	94.1	2558	9	US-10-176-757-103
18	25.4	94.1	2558	9	US-10-176-913-103
19	25.4	94.1	2558	9	US-10-180-552-103

20	25.4	94.1	2558	9	US-10-180-557-103	Sequence 103, App
21	25.4	94.1	2558	9	US-10-173-700-103	Sequence 103, App
22	25.4	94.1	2558	9	US-10-174-572-103	Sequence 103, App
23	25.4	94.1	2558	9	US-10-174-579-103	Sequence 103, App
24	25.4	94.1	2558	9	US-10-174-582-103	Sequence 103, App
25	25.4	94.1	2558	9	US-10-174-588-103	Sequence 103, App
26	25.4	94.1	2558	9	US-10-175-739-103	Sequence 103, App
27	25.4	94.1	2558	9	US-10-175-740-103	Sequence 103, App
28	25.4	94.1	2558	9	US-10-175-743-103	Sequence 103, App
29	25.4	94.1	2558	9	US-10-176-488-103	Sequence 103, App
30	25.4	94.1	2558	9	US-10-176-492-103	Sequence 103, App
31	25.4	94.1	2558	9	US-10-176-747-103	Sequence 103, App
32	25.4	94.1	2558	9	US-10-176-750-103	Sequence 103, App
33	25.4	94.1	2558	9	US-10-176-985-103	Sequence 103, App
34	25.4	94.1	2558	9	US-10-176-987-103	Sequence 103, App
35	25.4	94.1	2558	9	US-10-176-991-103	Sequence 103, App
36	25.4	94.1	2558	9	US-10-176-992-103	Sequence 103, App
37	25.4	94.1	2558	9	US-10-176-993-103	Sequence 103, App
38	25.4	94.1	2558	9	US-10-184-658-103	Sequence 103, App
39	25.4	94.1	2558	9	US-10-173-695-103	Sequence 103, App
40	25.4	94.1	2558	9	US-10-173-697-103	Sequence 103, App
41	25.4	94.1	2558	9	US-10-173-705-103	Sequence 103, App
42	25.4	94.1	2558	9	US-10-174-576-103	Sequence 103, App
43	25.4	94.1	2558	9	US-10-174-585-103	Sequence 103, App
44	25.4	94.1	2558	9	US-10-174-586-103	Sequence 103, App
45	25.4	94.1	2558	9	US-10-175-747-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-09-821-734-14
; Sequence 14, Application US/09821734
; Publication No. US20030027246A1
; GENERAL INFORMATION:
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Artur
; APPLICANT: Sia, Charles Dwo Yuan
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane
; TITLE OF INVENTION: (PSMA) and Uses Thereof
; FILE REFERENCE: 11014-22
; CURRENT APPLICATION NUMBER: US/09/821,734
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,386
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CLP330

Query Match 100.0%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGTCCTGTTG 27
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Db 1 GAGCTAGCACATTATGATGTCCTGTTG 27

RESULT 2
US-09-925-300-131
; Sequence 131, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

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; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 866
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (683)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (723)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (740)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (793)
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; NAME/KEY: misc feature
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; LOCATION: (841)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-300-131
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Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 535 GAGCTAGCACATTATGATGTCCTGTTG 561
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RESULT 3
US-10-094-699-2
; Sequence 2, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: CTLIMM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-094-699-2
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Query Match 100.0%; Score 27; DB 9; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 586 GAGCTAGCACATTATGATGTCCTGTTG 612
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RESULT 4
US-09-969-708-536
; Sequence 536, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
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; SEQ ID NO 536
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; TYPE: DNA
; ORGANISM: Homosapiens
US-09-969-708-536
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Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 586 GAGCTAGCACATTATGATGTCCTGTTG 612
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RESULT 5
US-09-978-295A-617
; Sequence 617, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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GenCore version 5.1.1.3
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(without alignments)
527.795 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	em_esthum:*
3:	em_estin:*
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6:	em_estpl:*
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10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	27	100.0	785	9	AI525231	AI525231 pt1.1-2.C
5	27	100.0	809	9	AI525228	AI525228 pt1.1-2.C
6	27	100.0	949	9	AL563971	AL563971 AL563971

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	8	25.4	94.1	882	14	BQ708386	BQ708386 AGENCOURT
	9	25.4	94.1	902	14	BQ708480	BQ708480 AGENCOURT
	10	25.4	94.1	904	14	BQ893679	BQ893679 AGENCOURT
	11	25.4	94.1	909	14	BQ948549	BQ948549 AGENCOURT
	12	25.4	94.1	914	14	BQ712611	BQ712611 AGENCOURT
	13	25.4	94.1	917	14	BQ711571	BQ711571 AGENCOURT
	14	25.4	94.1	937	14	BQ894290	BQ894290 AGENCOURT
	15	25.4	94.1	939	14	BQ712351	BQ712351 AGENCOURT
	16	25.4	94.1	998	14	BQ711650	BQ711650 AGENCOURT
	17	25.4	94.1	1187	14	BM926125	BM926125 AGENCOURT
C	18	19.8	73.3	578	17	AQ256048	AQ256048 nbxb0015E
	19	19.6	72.6	303	10	BB447160	BB447160 BB447160
C	20	19.6	72.6	415	13	BI621738	BI621738 RH53137.5
C	21	19.6	72.6	415	13	BI622365	BI622365 RH54225.5
C	22	19.6	72.6	468	9	AI957386	AI957386 fc90c08.x
C	23	19.6	72.6	653	17	AQ320303	AQ320303 RPCI11-10
C	24	19.6	72.6	769	10	AW019789	AW019789 fd46d07.x
C	25	19	70.4	333	13	BM385103	BM385103 UI-R-CN1-
C	26	19	70.4	411	10	BE210798	BE210798 so53f11.y
C	27	19	70.4	502	17	AQ623423	AQ623423 HS_5357_B
C	28	19	70.4	609	17	DR5C23T	AL733052 Danio rer
C	29	19	70.4	657	10	BE329924	BE329924 so71c08.y
C	30	19	70.4	710	13	BJ166802	BJ166802 BJ166802
C	31	19	70.4	968	17	CNS06XVK	AL420246 T3 end of
	32	19	70.4	996	12	BG339671	BG339671 602437241
	33	18.6	68.9	371	10	BB792813	BB792813 BB792813
	34	18.6	68.9	549	14	BQ081352	BQ081352 san23c10.
	35	18.6	68.9	619	13	BI434493	BI434493 EST537254
	36	18.6	68.9	708	12	BG125123	BG125123 EST470769
C	37	18.6	68.9	752	17	AG029187	AG029187 Pan trogl
	38	18.6	68.9	782	12	BG351593	BG351593 129B03 Ma
	39	18.6	68.9	1776	17	AG079557	AG079557 Pan trogl
	40	18.2	67.4	156	17	AZ459269	AZ459269 1M0263022
	41	18.2	67.4	208	14	BQ196926	BQ196926 NXLV107_B
	42	18.2	67.4	385	17	AQ096129	AQ096129 HS_3030_A
C	43	18.2	67.4	444	12	BG240159	BG240159 OV1_18_F0
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C	45	18.2	67.4	643	12	BF796866	BF796866 602258237

ALIGNMENTS

RESULT 1
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LOCUS AW898913 420 bp mRNA linear EST 24-MAY-2000
DEFINITION CM0-NN0079-140400-334-f10 NN0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW898913
VERSION AW898913.1 GI:8063118
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 420)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&tl2=CMO-NN0079-140
400-334-f10&tl3=2000-04-14&tl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 420.

FEATURES

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/db_xref="taxon:9606"
/clone_lib="NN0079"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
118 a 100 c 89 g 113 t

BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGTCCTGTTG 27
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Db 328 GAGCTAGCACATTATGATGTCCTGTTG 354

RESULT 2

AW473087/c
LOCUS

DEFINITION xp68c02.x2 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745506 3'
similar to gb:M99487 PROSTATE-SPECIFIC MEMBRANE ANTIGEN (HUMAN);,
mRNA sequence.

ACCESSION

VERSION
KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 385.

FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:2745506"
/clone_lib="NCI_CGAP_Ov39"
/sex="female"
/tissue_type="papillary serous ovarian metastasis"
/lab_host="DH10B"

/note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT
priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. CDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."

BASE COUNT 144 a 85 c 110 g 156 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 269 GAGCTAGCACATTATGATGTCCTGTTG 243

RESULT 3

BI772735

LOCUS

DEFINITION BI772735 603053273F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5202715 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1508 row: a column: 20

High quality sequence start: 5

High quality sequence stop: 703.

FEATURES

source

1..704
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/db_xref="taxon:9606"

/clone="IMAGE:5202715"

/clone_lib="NIH_MGC_122"

/lab_host="DH10B"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

BASE COUNT 184 a 168 c 174 g 178 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGTCCTGTTG 27

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:31:34 ; Search time 523.667 Seconds
(without alignments)
1500.527 Million cell updates/sec

Title: US-09-821-734-15
Perfect score: 27
Sequence: 1 ctgatgtacagcttggtacacaccta 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

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- 2: gb_htg:*
- 3: gb_in:*
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- 14: gb_vi:*
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- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
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- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	27	6	AX268377	AX268377 Sequence
2	27	100.0	2253	6	AX467227	AX467227 Sequence
3	27	100.0	2253	9	AY101595	AY101595 Homo sapi
4	27	100.0	2472	9	BC025672	BC025672 Homo sapi
5	27	100.0	2518	9	AF176574	AF176574 Homo sapi
6	27	100.0	2558	6	AX376036	AX376036 Sequence
7	27	100.0	2653	6	AX337498	AX337498 Sequence
8	27	100.0	2653	6	I23794	I23794 Sequence 1
9	27	100.0	2653	9	HUMPSM	M99487 Human prost
10	27	100.0	93525	9	AF007544	AF007544 Homo sapi
11	27	100.0	156255	2	AP002369	AP002369 Homo sapi
12	27	100.0	157527	9	AC117746	AC117746 Homo sapi
13	27	100.0	158524	2	AL162372	AL162372 Homo sapi
14	27	100.0	187638	2	AC118273	AC118273 Homo sapi
15	27	100.0	246865	2	AC074003	AC074003 Homo sapi
16	25.4	94.1	1992	9	AF261715	AF261715 Homo sapi
17	25.4	94.1	2061	6	AX403107	AX403107 Sequence
18	25.4	94.1	137888	9	AP003122	AP003122 Homo sapi
19	25.4	94.1	192648	2	AC024234	AC024234 Homo sapi
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21	22.2	82.2	2259	10	AF513486	AF513486 Rattus no
22	22.2	82.2	2348	10	AF040256	AF040256 Rattus no
23	22.2	82.2	2532	4	AF050502	AF050502 Sus scrof
24	22.2	82.2	2603	10	AF026380	AF026380 Mus muscu
25	22.2	82.2	2899	10	RN075973	U75973 Rattus norv
26	22.2	82.2	221969	2	AC106532	AC106532 Rattus no
27	22.2	82.2	235731	2	AC097423	AC097423 Rattus no
28	20.2	74.8	137922	2	AC073398	AC073398 Homo sapi
29	20.2	74.8	155533	9	AC079177	AC079177 Homo sapi
30	19.8	73.3	96460	9	HS633020	AL023804 Human DNA
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32	19.6	72.6	61411	2	AC106846	AC106846 Homo sapi
33	19.6	72.6	99183	9	AL360091	AL360091 Human DNA
34	19.6	72.6	162704	2	AC016289	AC016289 Homo sapi
35	19.6	72.6	187693	2	AP001502	AP001502 Homo sapi
36	19.6	72.6	199347	2	AL805952	AL805952 Mus muscu
37	19.6	72.6	205237	2	AL807399	AL807399 Mus muscu
38	19.6	72.6	208160	2	AC124254	AC124254 Homo sapi
39	19.6	72.6	212553	2	AC099581	AC099581 Mus muscu
40	19.4	71.9	2004	1	ASU09240	U09240 Anabaena sp
41	19.4	71.9	2004	1	S76266	S76266 fraC=Frac l
42	19.4	71.9	341880	1	AP003589	AP003589 Nostoc sp
43	19.2	71.1	468	1	AF190908	AF190908 Xanthomon
44	19.2	71.1	150017	2	AL773509	AL773509 Mus muscu
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ALIGNMENTS

RESULT 1	AX268377	AX268377	Sequence 15 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
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DEFINITION	AX268377	Sequence 15 from Patent WO0174845.					
ACCESSION	AX268377	Sequence 15 from Patent WO0174845.					
VERSION	AX268377.1	GI:16541584					
KEYWORDS		synthetic construct.					
SOURCE		synthetic construct					
ORGANISM		artificial sequences.					
REFERENCE	1						
AUTHORS		Pedyczak,A., Chong,P. and Sia,C.D.					
TITLE		Immunogenic peptides derived from prostate-specific membrane antigen (psma) and uses thereof					
JOURNAL		Patent: WO 0174845-A 15 11-OCT-2001;					

Pred. No. is the number of results predicted by chance to have a

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Aventis Pasteur Limited (CA)
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LOCUS
DEFINITION Sequence 1 from Patent WO0234287.
ACCESSION AX467227
VERSION AX467227.1 GI:21900509
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Beier,A.M., Gautam,A. and Mouritsen,S.R.
TITLE Novel therapeutic vaccine formulations
JOURNAL Patent: WO 0234287-A 1 02-MAY-2002;
Pharmexa A/S (DK)
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Best Local Similarity 100.0%; Pred. No. 0.0055;
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LOCUS
DEFINITION 2253 bp mRNA linear PRI 27-MAY-2002
ACCESSION AY101595
VERSION AY101595.1 GI:21217742
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2253)
AUTHORS Ye,C.Z., Zhang,F.L., Zhang,Y.K. and Chen,C.Q.
TITLE Cloning and sequencing of Chinese prostate-specific membrane
antigen
JOURNAL Mianyixue zazhi 17 (5), 328-330 (2001)
REFERENCE 2 (bases 1 to 2253)
AUTHORS Ye,C.Z.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) Department of Urology, Zhongshan Hospital,
Medical Center of Fudan University, Fenglin Rd 180, Shanghai
200032, China
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Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS
DEFINITION 2472 bp mRNA linear PRI 11-MAR-2002
ACCESSION BC025672
VERSION BC025672.1 GI:19343603
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 Seconds
(without alignments)
614.181 Million cell updates/sec

Title: US-09-821-734-15
Perfect score: 27
Sequence: 1 ctgatgtacagcttggtacacaaccta 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	100.0	27	22 AAS15142	Human DNA encoding
2	27	100.0	1037	21 AAF15651	Human prostate can
3	27	100.0	2226	21 AAA12732	DNA encoding a hum
4	27	100.0	2253	21 AAA09454	Human prostate spe
5	27	100.0	2558	21 AAC78599	Human PRO739 nucle
6	27	100.0	2558	22 AAS45976	Human DNA encoding
7	27	100.0	2653	15 AAQ65520	Prostate-specific
8	27	100.0	2653	24 ABK86204	cDNA encoding huma
9	27	100.0	2653	24 ABK64556	Human benign prost

10	27	100.0	2653	24 ABL69670	Prostate cancer re
11	27	100.0	2654	17 AAT36785	Prostate-specific
12	27	100.0	2884	23 ABV22873	Human prostate exp
13	27	100.0	2884	23 ABV23013	Human prostate exp
14	27	100.0	2884	23 ABV28703	Human prostate exp
15	27	100.0	2884	23 ABV28849	Human prostate exp
16	25.4	94.1	37	22 AAD17672	PCR primer #1 used
17	25.4	94.1	1992	21 AAC61762	cDNA encoding a pr
18	25.4	94.1	2061	24 AAD34009	Human gene 4 cDNA.
19	25	92.6	656	21 AAF15621	Human prostate can
20	22.2	82.2	2082	21 AAA09459	Murine prostate sp
21	22.2	82.2	2256	21 AAA09458	Murine prostate sp
22	20.8	77.0	36	22 AAD17673	PCR primer #2 used
23	19.8	73.3	1843	21 AAA61051	Maize embryo speci
24	19.8	73.3	6694	21 AAA61053	Maize embryo speci
25	18.6	68.9	128139	24 AAI64291	RRV genome nucleot
26	18.6	68.9	133719	21 AAC64754	Macaca mulatta rha
27	18	66.7	1356	20 AAX20570	Polynucleotide seq
28	18	66.7	1359	24 ABL01520	Murine apoptosis r
29	18	66.7	5752	22 AAF85087	Nucleotide sequenc
30	17.8	65.9	275	16 AAT24115	Human gene signatu
31	17.8	65.9	1006	21 AAC77762	Human cancer assoc
32	17.8	65.9	4362	22 AAL05795	Human reproductive
33	17.8	65.9	4362	23 ABK72136	Human ovarian anti
34	17.8	65.9	4362	23 ABL98359	Human testicular a
35	17.8	65.9	4362	24 ABK91728	Novel ovarian rela
36	17.6	65.2	363	21 AAC17262	Human secreted pro
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39	17.6	65.2	599	24 ABN64935	Human cancer relat
40	17.6	65.2	2314	22 AAS21301	Human cDNA sequenc
41	17.6	65.2	2930	22 AAF72750	Human prostate can
42	17.6	65.2	4740	22 AAI57867	Human polynucleoti
43	17.4	64.4	400	24 ABN94600	Gene #1098 used to
44	17.4	64.4	421	22 ABA56490	Human foetal liver
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ALIGNMENTS

RESULT 1

AAS15142

ID AAS15142 standard; DNA; 27 BP.

XX AAS15142;

AC AAS15142;

XX 16-JAN-2002 (first entry)

DE Human DNA encoding a PSMA derived immunogenic peptide CLP333.

XX Human; ds; PSMA; prostate specific membrane antigen; prostate cancer; tumour; immunogenic peptide; cytostatic; gene therapy; CLP333.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..27

FT /*tag= a

FT /product= "CLP333"

FT /partial

FT /note= "No start or stop codon"

XX WO200174845-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-CA00411.

XX 31-MAR-2000; 2000US-193386P.

PA (AVET) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sia CDY;
XX
DR WPI; 2001-626378/72.
DR P-PSDB; AAU09107.
XX
PT New polypeptides useful for inducing an immune response and treating
PT prostate cancer comprises polypeptides derived from the prostate
PT specific membrane antigen -
XX
XX
PS Claim 6; Page 15; 47pp; English.
XX
CC The invention relates to prostate specific membrane antigen (PSMA)
CC derived peptides (and the nucleic acids encoding them) capable of
CC eliciting an immune response. The molecules of the invention are used to
CC elicit an immune response, particularly to treat cancer and tumours,
CC especially prostate cancer. Delivery of the peptides may be by
CC expression from the nucleic acids encoding them (i.e. gene therapy).
CC The present sequence encodes a PSMA derived immunogenic peptide.
XX
SQ Sequence 27 BP; 8 A; 7 C; 5 G; 7 T; 0 other;

Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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ID AAF15651 standard; cDNA; 1037 BP.
XX
AC AAF15651;
XX
DT 13-MAR-2001 (first entry)
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:86.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05988.
PF
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PR 12-MAR-1999; 99US-0124270.
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PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR P-PSDB; AAB56448.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
PS Claim 1; Page 672-673; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.

CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 1037 BP; 337 A; 174 C; 228 G; 297 T; 1 other;

Query Match 100.0%; Score 27; DB 21; Length 1037;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACAACCTA 27
Db 53 CTGATGTACAGCTTGGTACACAACCTA 79

RESULT 3
AAAL2732
ID AAAL2732 standard; DNA; 2226 BP.
XX
AC AAAL2732;
XX
DT 25-JUL-2000 (first entry)
DE DNA encoding a human prostate specific membrane antigen.
XX
KW Human; prostate specific membrane antigen; inactive antigen; cancer;
KW prostate cancer; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2226
FT /*tag= a
FT /product= "prostate specific membrane antigen"
XX
PN WO200018933-A1.
XX
PD 06-APR-2000.
XX
PF 09-SEP-1999; 99WO-US20508.
XX
PR 30-SEP-1998; 98US-0164034.
XX
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUNB/) ZOUNBAK S.
XX
PI Mincheff MS, Loukinov DI, Zoubak S;
XX
DR WPI; 2000-293166/25.
DR P-PSDB; AAY84667.
XX
PT New DNA constructs expressing functionally inactive, altered antigens
PT are used for treating prostate cancer -
XX
PS Claim 8; Page 16-18; 23pp; English.
XX
CC The present sequence encodes a human prostate specific membrane
CC antigen. The polynucleotide is used to construct the DNA constructs of
CC the invention. The specification describes DNA constructs which cause
CC expression of functionally inactive, altered antigens which are
CC unaltered with respect to the efficiency of transcription and
CC translation of DNA, translation of RNA or the generation of antigenic

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds
(without alignments)
394.299 Million cell updates/sec

Title: US-09-821-734-15
Perfect score: 27
Sequence: 1 ctgatgtacagcttggtacacaaccta 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	2133	4	US-09-164-034B-1
2	27	100.0	2653	1	US-08-325-553-1
3	27	100.0	2653	2	US-08-394-152A-1
4	17.2	63.7	5769	1	US-08-652-971-1
5	17.2	63.7	5769	2	US-08-991-258A-1
6	17.2	63.7	5769	2	US-08-769-399-1
7	17.2	63.7	5769	3	US-08-991-953A-1
8	17.2	63.7	112132	4	US-09-741-150-3
9	16.6	61.5	1952	2	US-08-481-337A-7
10	16.6	61.5	1952	4	US-09-382-256-17
11	16.6	61.5	1952	4	US-09-395-115-17
12	16.6	61.5	1952	4	US-08-436-265-17
13	16.6	61.5	1952	4	US-09-679-187-17
14	16.6	61.5	1952	5	PCT-US95-05467-7
15	16.6	61.5	2056	4	US-08-158-735A-1
16	16.6	61.5	2070	4	US-09-382-256-13
17	16.6	61.5	2070	4	US-09-395-115-13
18	16.6	61.5	2070	4	US-08-436-265-13
19	16.6	61.5	2070	4	US-09-679-187-13
20	16.6	61.5	2076	4	US-08-123-934A-3
21	16.6	61.5	2076	5	PCT-US94-10080-3
22	16.6	61.5	2252	4	US-08-462-467B-13
23	16.6	61.5	2252	4	US-08-334-179A-13
24	16.6	61.5	2402	4	US-08-462-467B-11
25	16.6	61.5	2402	4	US-08-158-735A-3
26	16.6	61.5	2402	4	US-08-334-179A-11
27	16.4	60.7	330	2	US-08-437-013-4

28	16.4	60.7	641	2	US-08-437-013-1	Sequence 1, Appli
29	16.4	60.7	641	2	US-08-437-013-28	Sequence 28, Appl
30	16.4	60.7	709	2	US-08-437-013-26	Sequence 26, Appl
31	16.4	60.7	1965	4	US-09-227-717-1	Sequence 1, Appli
32	16.4	60.7	5014	4	US-09-381-862-3	Sequence 3, Appli
33	16.4	60.7	4403765	4	US-09-103-840A-2	Sequence 2, Appli
34	16.4	60.7	4411529	4	US-09-103-840A-1	Sequence 1, Appli
35	16.2	60.0	4203	2	US-08-288-630-3	Sequence 3, Appli
36	16	59.3	536	4	US-09-347-819-7	Sequence 7, Appli
37	16	59.3	1001	4	US-09-641-638-470	Sequence 470, App
38	16	59.3	1245	4	US-09-134-001C-2691	Sequence 2691, Ap
39	16	59.3	3490	2	US-08-841-483-3	Sequence 3, Appli
40	16	59.3	3490	4	US-09-382-911-3	Sequence 3, Appli
41	16	59.3	4094	2	US-08-841-483-5	Sequence 5, Appli
42	16	59.3	4094	4	US-09-382-911-5	Sequence 5, Appli
43	15.8	58.5	1194	4	US-09-134-001C-1267	Sequence 1267, Ap
44	15.8	58.5	1261	3	US-08-967-272-1	Sequence 1, Appli
45	15.8	58.5	2832	4	US-08-476-515A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-164-034B-1
; GENERAL INFORMATION:
; APPLICANT: Mincheff, Milcho S.
; Loukinov, I. Dmitri
; Zoubak, Serguei
; TITLE OF INVENTION: Immunotherapy of Cancer Through Expression
; of Truncated Tumor- or Tumor-Associated Antigen
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William S. Ramsey,
; Ramsey, Cook, Looper & Kurlander, LLC
; STREET: 10420 Little Patuxent Parkway, Suite 250
; CITY: Columbia
; STATE: Maryland
; COUNTRY: USA
; ZIP: 21044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/164,034B
; FILING DATE: 30-Sep-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramsey, William S.
; REGISTRATION NUMBER: 32,715
; REFERENCE/DOCKET NUMBER: bril
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (410) 992-9660
; TELEFAX: (410) 992-9540
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-164-034B-1

Query Match 100.0%; Score 27; DB 4; Length 2133;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTA 27
|||||
Db 1279 CTGATGTACAGCTTGGTACACACCTA 1305

RESULT 2
US-08-325-553-1
; Sequence 1, Application US/08325553
; Patent No. 5538866
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.

APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTA 27
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Db 1666 CTGATGTACAGCTTGGTACACACCTA 1692

RESULT 3
US-08-394-152A-1
Sequence 1, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
US THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1666 CTGATGTACAGCTTGGTACACACCTA 1692

RESULT 4
US-08-652-971-1
Sequence 1, Application US/08652971
Patent No. 5814507
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
FILING DATE:

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds
(without alignments)
703.471 Million cell updates/sec

Title: US-09-821-734-15
Perfect score: 27
Sequence: 1 ctgatgtacagcttggtacacaacctta 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	27	100.0	27	9	US-09-821-734-15
2	27	100.0	1037	10	US-09-925-300-86
3	27	100.0	2558	9	US-09-978-295A-617
4	27	100.0	2558	9	US-09-978-697-617
5	27	100.0	2558	9	US-09-978-192A-617
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8	27	100.0	2558	9	US-10-174-590-103
9	27	100.0	2558	9	US-10-176-758-103
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13	27	100.0	2558	9	US-10-175-752-103
14	27	100.0	2558	9	US-10-176-482-103
15	27	100.0	2558	9	US-10-176-757-103
16	27	100.0	2558	9	US-10-176-913-103
17	27	100.0	2558	9	US-10-180-522-103
18	27	100.0	2558	9	US-10-180-557-103
19	27	100.0	2558	9	US-10-173-700-103

20	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
24	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-743-103	Sequence 103, App
27	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
28	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
29	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
36	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
37	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
40	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
42	27	100.0	2558	9	US-10-174-586-103	Sequence 103, App
43	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
44	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-485-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-09-821-734-15
; Sequence 15, Application US/09821734
; Publication No. US20030027246A1
; GENERAL INFORMATION:
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Artur
; APPLICANT: Sia, Charles Dwo Yuan
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane
; TITLE OF INVENTION: (PSMA) and Uses Thereof
; FILE REFERENCE: 11014-22
; CURRENT APPLICATION NUMBER: US/09/821,734
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,386
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CLP333
US-09-821-734-15

Query Match 100.0%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACAACCTA 27
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Db 1 CTGATGTACAGCTTGGTACACAACCTA 27

RESULT 2
US-09-925-300-86
; Sequence 86, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 86
LENGTH: 1037
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-300-86

Query Match 100.0%; Score 27; DB 10; Length 1037;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTA 27
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Db 53 CTGATGTACAGCTTGGTACACACCTA 79

RESULT 3

US-09-978-295A-617
Sequence 617, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
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PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:33:49 ; Search time 828.5 Seconds
(without alignments)
527.795 Million cell updates/sec

Title: US-09-821-734-15
Perfect score: 27
Sequence: 1 ctgatgtacagcttggtacacaaccta 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	296	9 AA371450	AA371450 EST83235
2	27	100.0	474	10 AW945136	AW945136 EST361329
3	27	100.0	563	10 AW951407	AW951407 EST363477
4	27	100.0	625	12 BG206102	BG206102 RST25537
5	27	100.0	767	12 BG194269	BG194269 RST13413
6	27	100.0	938	9 AL532732	AL532732 AL532732

C	7	27	100.0	1019	9	AL532691	AL532691
	8	22.2	82.2	459	9	AI892895	AI892895 mq24h05.y
C	9	22.2	82.2	464	9	AI647690	AI647690 uk37h10.x
	10	22.2	82.2	662	9	AA116793	AA116793 mq24h05.r
	11	22.2	82.2	3003	11	AK002920	AK002920 Mus muscu
C	12	20.6	76.3	278	9	AI788531	AI788531 uk46b04.x
	13	19.6	72.6	874	12	BG831345	BG831345 602766192
C	14	19.6	72.6	874	13	BI908012	BI908012 603068967
C	15	19.2	71.1	610	17	FR0028442	AL024814 Fugu rubr
C	16	19.2	71.1	653	17	CNS07600	AL430798 clone XBA
	17	19.2	71.1	705	17	BH176186	BH176186 005_D_06-
	18	19.2	71.1	705	17	CNS07J05	AL613127 T3 end of
C	19	19.2	71.1	710	10	AV979798	AV979798 AV979798
	20	19	70.4	527	13	BJ221163	BJ221163 BJ221163
C	21	18.8	69.6	536	10	BB728352	BB728352 BB728352
C	22	18.8	69.6	1289	14	BQ718347	BQ718347 AGENCOURT
	23	18.6	68.9	400	9	AL837844	AL837844 AL837844
	24	18.6	68.9	435	13	BJ074589	BJ074589 BJ074589
C	25	18.6	68.9	457	17	AQ812530	AQ812530 HS_5249_B
C	26	18.6	68.9	460	17	AQ513855	AQ513855 HS_5152_A
	27	18.6	68.9	514	13	BJ061531	BJ061531 BJ061531
	28	18.6	68.9	514	13	BJ066254	BJ066254 BJ066254
	29	18.6	68.9	554	13	BJ061747	BJ061747 BJ061747
	30	18.6	68.9	566	13	BJ052567	BJ052567 BJ052567
C	31	18.6	68.9	583	10	BE192345	BE192345 db91a04.x
	32	18.6	68.9	594	10	AV951122	AV951122 AV951122
	33	18.6	68.9	594	13	BJ064305	BJ064305 BJ064305
	34	18.6	68.9	630	13	BJ096767	BJ096767 BJ096767
	35	18.6	68.9	636	13	BJ072058	BJ072058 BJ072058
	36	18.6	68.9	639	13	BJ074118	BJ074118 BJ074118
	37	18.6	68.9	649	17	BH277517	BH277517 CH230-84B
	38	18.6	68.9	677	12	BG162353	BG162353 de33901.y
	39	18.6	68.9	923	14	BQ724752	BQ724752 AGENCOURT
	40	18.6	68.9	1079	12	BF796799	BF796799 602259748
C	41	18.4	68.1	689	9	AI788829	AI788829 uk54e07.x
	42	18.2	67.4	253	10	AW317248	AW317248 sg46a02.y
	43	18.2	67.4	544	12	BG873877	BG873877 MEST43-F1
	44	18.2	67.4	612	9	AL634736	AL634736 AL634736
	45	18.2	67.4	638	14	BQ522172	BQ522172 NISC_nll5

ALIGNMENTS

RESULT 1	AA371450	AA371450	296 bp	mRNA	linear	EST 21-APR-1997
LOCUS	EST83235	Prostate gland I Homo sapiens	cdna 5'	end similar to		
DEFINITION	prostate-specific membrane antigen, mRNA sequence.					
ACCESSION	AA371450					
VERSION	AA371450.1	GI:2023767				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and					

TITLE Venter, J.C.
JOURNAL Initial assessment of human gene diversity and expression patterns
MEDLINE based upon 83 million nucleotides of cDNA sequence
COMMENT Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other_ESTs: THC166946
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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/organism="Homo sapiens"
/db_xref="ATCC (inhost):175848"
/db_xref="taxon:9606"
/clone_lib="Prostate gland I"
/sex="male"
/dev_stage="adult, 21 yrs"
/note="Organ: prostate; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
BASE COUNT 98 a 58 c 66 g 73 t 1 others
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Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTA 27
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Db 53 CTGATGTACAGCTTGGTACACACCTA 79

RESULT 2
AW945136
LOCUS 474 bp mRNA linear EST 31-MAY-2000
DEFINITION MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION AW945136
VERSION AW945136.1 GI:8122887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 0
Seq primer: Reverse.

FEATURES
source
1..474
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGA"
/note="Vector: pBluescriptSKm"
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Query Match 100.0%; Score 27; DB 10; Length 474;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTA 27
|||||
Db 52 CTGATGTACAGCTTGGTACACACCTA 78

RESULT 3
AW951407
LOCUS 563 bp mRNA linear EST 01-JUN-2000
DEFINITION MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
ACCESSION AW951407
VERSION AW951407.1 GI:8141080
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 563)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 27
Seq primer: Reverse.

FEATURES
source
1..563
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGB"
/note="Vector: pBluescriptSKm"
BASE COUNT 179 a 102 c 121 g 160 t 1 others
ORIGIN

Query Match 100.0%; Score 27; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTA 27
|||||
Db 52 CTGATGTACAGCTTGGTACACACCTA 78

RESULT 4
BG206102
LOCUS 625 bp mRNA linear EST 21-APR-2001
DEFINITION Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG206102
VERSION BG206102.1 GI:13727789
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 625)
AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith
E., Veloso, N., Klika, A., Hess, J., Cuthren, K., Lo, K., Offenbacher
J., Danzig, J. and Ducar, M.

TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:31:34 ; Search time 523.667 Seconds
(without alignments)
1500.527 Million cell updates/sec

Title: US-09-821-734-16
Perfect score: 27
Sequence: 1 atgatgaatgatcaactcatgtttctg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :					GenEmbl:				
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					2:	gb_htg:	*		
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					4:	gb_om:	*		
					5:	gb_ov:	*		
					6:	gb_pat:	*		
					7:	gb_ph:	*		
					8:	gb_pl:	*		
					9:	gb_pr:	*		
					10:	gb_ro:	*		
					11:	gb_sts:	*		
					12:	gb_sy:	*		
					13:	gb_un:	*		
					14:	gb_vi:	*		
					15:	em_ba:	*		
					16:	em_fun:	*		
					17:	em_hum:	*		
					18:	em_in:	*		
					19:	em_mu:	*		
					20:	em_om:	*		
					21:	em_or:	*		
					22:	em_ov:	*		
					23:	em_pat:	*		
					24:	em_ph:	*		
					25:	em_pl:	*		
					26:	em_ro:	*		
					27:	em_sts:	*		
					28:	em_un:	*		
					29:	em_vi:	*		
					30:	em_htg_hum:	*		
					31:	em_htg_inv:	*		
					32:	em_htg_other:	*		
					33:	em_htg_mus:	*		
					34:	em_htg_pln:	*		
					35:	em_htg_rod:	*		
					36:	em_htg_mam:	*		
					37:	em_htg_vrt:	*		
					38:	em_sy:	*		
					39:	em_htgo_hum:	*		
					40:	em_htgo_mus:	*		
					41:	em_htgo_other:	*		

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	100.0	27	6	AX268378	AX268378 Sequence
2	27	100.0	1992	9	AF261715	AF261715 Homo sapi
3	27	100.0	2061	6	AX403107	AX403107 Sequence
4	27	100.0	2253	6	AX467227	AX467227 Sequence
5	27	100.0	2253	9	AY101595	AY101595 Homo sapi
6	27	100.0	2518	9	AF176574	AF176574 Homo sapi
7	27	100.0	2558	6	AX376036	AX376036 Sequence
8	27	100.0	2653	6	AX337498	AX337498 Sequence
9	27	100.0	2653	6	I23794	I23794 Sequence 1
10	27	100.0	2653	9	HUMPSM	M99487 Human prost
11	27	100.0	67466	2	AC103729	AC103729 Homo sapi
12	27	100.0	67466	2	AC103729	AC103729 Homo sapi
13	27	100.0	93525	9	AF007544	AF007544 Homo sapi
14	27	100.0	137888	9	AP003122	AP003122 Homo sapi
15	27	100.0	156255	2	AP002369	AP002369 Homo sapi
16	27	100.0	157527	9	AC117746	AC117746 Homo sapi
17	27	100.0	158524	2	AL162372	AL162372 Homo sapi
18	27	100.0	187638	2	AC118273	AC118273 Homo sapi
19	27	100.0	192648	2	AC024234	AC024234 Homo sapi
20	27	100.0	246865	2	AC074003	AC074003 Homo sapi
21	23.8	88.1	170102	9	AC009237	AC009237 Homo sapi
22	22.2	82.2	2532	4	AF050502	AF050502 Sus scrof
23	21.8	80.7	66084	8	AB015468	AB015468 Arabidops
24	21.2	78.5	73794	2	AC101544	AC101544 Mus muscu
25	21.2	78.5	182240	2	AC131039	AC131039 Mus muscu
26	20.8	77.0	180812	2	AC127403	AC127403 Rattus no
27	20.6	76.3	3152	6	AX006438	AX006438 Sequence
28	20.6	76.3	3152	9	HSA012370	AJ012370 Homo sapi
29	20.6	76.3	3171	6	AX136153	AX136153 Sequence
30	20.6	76.3	91667	2	AP005435	AP005435 Homo sapi
31	20.6	76.3	120000	9	AP004607	AP004607 Homo sapi
32	20.6	76.3	149745	9	AP000648	AP000648 Homo sapi
33	20.6	76.3	166287	2	AC060830	AC060830 Homo sapi
34	20.6	76.3	168577	9	AP000827	AP000827 Homo sapi
35	20.6	76.3	173005	2	AP001769	AP001769 Homo sapi
36	20.6	76.3	189711	2	AC096944	AC096944 Rattus no
37	20.4	75.6	241280	2	AC020854	AC020854 Mus muscu
38	20.2	74.8	112375	2	AC120576	AC120576 Rattus no
39	20.2	74.8	113939	2	AP004052	AP004052 Oryza sat
40	20.2	74.8	122241	2	AP004129	AP004129 Oryza sat
41	20.2	74.8	150927	2	AP004756	AP004756 Oryza sat
42	20.2	74.8	182520	2	AC112304	AC112304 Rattus no
43	20.2	74.8	211023	2	AL807239	AL807239 Danio rer
44	19.8	73.3	106376	9	AL138714	AL138714 Human DNA
45	19.8	73.3	156806	2	AC021353	AC021353 Homo sapi

ALIGNMENTS

RESULT 1	AX268378	AX268378	Sequence 16 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268378	AX268378	AX268378				
DEFINITION	AX268378	AX268378	AX268378				
ACCESSION	AX268378	AX268378	AX268378				
VERSION	AX268378.1	AX268378.1	GI:16541585				
KEYWORDS	AX268378.1	AX268378.1	GI:16541585				
SOURCE	AX268378.1	AX268378.1	GI:16541585				
ORGANISM	AX268378.1	AX268378.1	GI:16541585				
REFERENCE	AX268378.1	AX268378.1	GI:16541585				
AUTHORS	AX268378.1	AX268378.1	GI:16541585				
TITLE	AX268378.1	AX268378.1	GI:16541585				
JOURNAL	AX268378.1	AX268378.1	GI:16541585				

FEATURES	Aventis Pasteur Limited (CA)																						
	Location/Qualifiers																						
source	1..27																						
	/organism="synthetic construct"																						
BASE COUNT	/db_xref="taxon:32630"																						
	/note="CLP336"																						
ORIGIN	8 a	4 c	5 g	10 t																			
Query Match	100.0%; Score 27; DB 6; Length 27;																						
	Best Local Similarity 100.0%; Pred. No. 0.32;																						
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;																						
QY	1	ATGATGAATGATCAACTCATGTTTCTG	27																				
Db																							
	1	ATGATGAATGATCAACTCATGTTTCTG	27																				
RESULT 2																							
	AF261715																						
LOCUS	1992 bp mRNA linear PRI 02-NOV-2000																						
	Homo sapiens prostate-specific membrane antigen-like protein																						
DEFINITION	(PSMAL/GCP III) mRNA, complete cds.																						
	AF261715																						
ACCESSION	AF261715.1 GI:11078563																						
VERSION																							
KEYWORDS																							
SOURCE	Homo sapiens.																						
	Homo sapiens																						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																						
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																						
REFERENCE	1 (bases 1 to 1992)																						
	O'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.																						
AUTHORS	Cloning and Characterization of a novel glutamate-preferring																						
	peptidase that maps to the SC2DII locus: a candidate gene for																						
TITLE	Schizophrenia?																						
	Unpublished																						
JOURNAL	2 (bases 1 to 1992)																						
	O'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.																						
REFERENCE	Expression Profile of Prostate-Specific Membrane Antigen (PSMA)																						
	versus a Prostate-Specific Membrane Antigen-Like Gene in Normal																						
AUTHORS	Tissues, Prostate Cancer and Tumor Associated-Vasculature																						
	Unpublished																						
JOURNAL	3 (bases 1 to 1992)																						
	O'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.																						
AUTHORS	Direct Submission																						
	Submitted (27-APR-2000) Cancer Biology, Cleveland Clinic																						
TITLE	Foundation, NB 40, 9500 Euclid Avenue, Cleveland, OH 44195, USA																						
	Location/Qualifiers																						
JOURNAL	1..1992																						
	/organism="Homo sapiens"																						
FEATURES	/db_xref="taxon:9606"																						
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CDS	/gene="PSMAL/GCP III"																						
	527..1855																						
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CDS	/note="glutamate carboxypeptidase III; similar to Homo																						
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gene	peptidase family; formed by duplication of the PSMA gene"																						
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CDS	TRIYNVIGTLRGAVEPDYVILGGHRSWVFGIDPQSGAAVWHETVRSFGTLKKEGW																						
	RPRRTILFASWDAEEFGLLGSTEAEDNSRLQERGVAYINADSSIEGNYTLRVDCTP																						
source	LMYSLVNLTKELKSPDEGEGKSLYESWTKSPSPFSGMPRIKSLGSGNDFEVFFQ																						
	RLGIASGRARYTKNWETNKFSGYPLYHSVYETVELVEKFDPMFKYHLTVQVRGGMV																						
CDS	FELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEMKTYLSLSDSLFSVAKNFTEI																						
FEATURES	ASKFSERLQDFDKSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKY																						
	AGESFPGIYDALFDIESKVDPSKAWGDKRKQISVAAFTVQAAAETLSEVA"																						
source	638 a																						
	352 c																						
BASE COUNT	451 g																						
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ORIGIN																							
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LOCUS	AX403107																						
	Sequence 2 from Patent WO0226984.																						
DEFINITION	AX403107																						
	AX403107																						
ACCESSION	AX403107.1 GI:21388049																						
VERSION																							
KEYWORDS	human.																						
	Homo sapiens																						
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																						
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																						
ORGANISM	1																						
	Betty,M., An,W., Ling,H.P. and Rhodes,K.																						
REFERENCE	Potassium channel interactors and uses therefor																						
AUTHORS	Patent: WO 0226984-A 2 04-APR-2002;																						
	MILLENNIUM PHARM INC (US)																						
TITLE	Location/Qualifiers																						
	1..2061																						
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VERSION																							
KEYWORDS	human.																						
	Homo sapiens																						
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																						
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																						
ORGANISM	1																						
	Beier,A.M., Gautam,A. and Mouritsen,S.R.																						
REFERENCE	Novel therapeutic vaccine formulations																						
AUTHORS	Patent: WO 0234287-A 1 02-MAY-2002;																						
	Pharmexa A/S (DK)																						
TITLE	Location/Qualifiers																						
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 Seconds
(without alignments)
614.181 Million cell updates/sec

Title: US-09-821-734-16
Perfect score: 27
Sequence: 1 atgatgaatgatcaactcatgtttctg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	442	ABK64577	Human benign prost
3	27	100.0	578	ABV43616	Human prostate exp
4	27	100.0	1037	AAF15651	Human prostate can
5	27	100.0	1992	AAC61762	cDNA encoding a pr
6	27	100.0	2061	AAD34009	Human gene 4 cDNA.
7	27	100.0	2226	AAA12732	DNA encoding a hum
8	27	100.0	2253	AAA09454	Human prostate spe
9	27	100.0	2558	AAC78599	Human PRO739 nucle

10	27	100.0	2558	22	AAS45976	Human DNA encoding
11	27	100.0	2653	15	AAQ65520	Prostate-specific
12	27	100.0	2653	24	ABK86204	cDNA encoding huma
13	27	100.0	2653	24	ABK64556	Human benign prost
14	27	100.0	2653	24	ABL69670	Prostate cancer re
15	27	100.0	2654	17	AAT36785	Prostate-specific
16	27	100.0	2884	23	ABV22873	Human prostate exp
17	27	100.0	2884	23	ABV23013	Human prostate exp
18	27	100.0	2884	23	ABV28703	Human prostate exp
19	27	100.0	2884	23	ABV28849	Human prostate exp
20	20.6	76.3	3110	21	AAZ58312	Human peptidase NA
21	20.6	76.3	3171	22	AAF933781	Human cDNA encodin
22	20.6	76.3	3771	22	AAH98667	Human EST-derived
23	19	70.4	249	24	ABL72340	Corn tassal-derive
24	19	70.4	678	24	ABN90915	Staphylococcus epi
25	19	70.4	723	24	ABK15070	Potato cDNA for hi
26	19	70.4	2082	21	AAA09459	Murine prostate sp
27	19	70.4	2256	21	AAA09458	Murine prostate sp
28	18.6	68.9	693	22	AAH04248	Human cDNA clone (
29	18.6	68.9	719	22	AAS30470	DNA encoding novel
30	18.6	68.9	719	22	AAI06250	Human reproductive
31	18.6	68.9	753	11	AAQ05733	Glutathione-S-tran
32	18.6	68.9	1862	22	AAH17257	Human cDNA sequenc
33	18.6	68.9	2548	21	AAZ35758	Strongylocentrotus
34	18.6	68.9	24789	23	ABL28640	Drosophila melanog
35	18.6	68.9	130480	22	AAF25833	R. marinus bacteri
36	18.4	68.1	16532	23	ABL12290	Drosophila melanog
37	18.2	67.4	910715	20	AAZ02048	Borrelia burgdorfe
38	18	66.7	27	22	AAS15149	Human DNA encoding
39	18	66.7	300	21	AAA00166	Human colon cancer
40	18	66.7	354	21	AAC18682	Human secreted pro
41	18	66.7	368	24	ABQ85523	Arabidopsis thalia
42	18	66.7	475	22	ABA52291	Human foetal liver
43	18	66.7	475	22	ABA22092	Probe #558 for gen
44	18	66.7	475	22	AAK00566	Human brain expres
45	18	66.7	475	22	AAK26015	Human bone marrow

ALIGNMENTS

RESULT 1
AAS15143
ID AAS15143 standard; DNA; 27 BP.

XX AAS15143;

AC AAS15143;

DT 16-JAN-2002 (first entry)

XX Human DNA encoding a PSMA derived immunogenic peptide CLP336.

DE Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;

XX tumour; immunogenic peptide; cytostatic; gene therapy; CLP336.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..27

FT /*tag= a

FT /product= "CLP336"

FT /partial

FT /note= "No stop codon"

XX WO200174845-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-CA00411.

XX 31-MAR-2000; 2000US-193386P.

XX (AVET) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sia CDY;
XX WPI; 2001-626378/72.
DR P-PSDB; AAU09108.
XX
PT New polypeptides useful for inducing an immune response and treating
PT prostate cancer comprises polypeptides derived from the prostate
PT specific membrane antigen.
XX
PS Claim 6; Page 15; 47pp; English.
XX
CC The invention relates to prostate specific membrane antigen (PSMA)
CC derived peptides (and the nucleic acids encoding them) capable of
CC eliciting an immune response. The molecules of the invention are used to
CC elicit an immune response, particularly to treat cancer and tumours,
CC especially prostate cancer. Delivery of the peptides may be by
CC expression from the nucleic acids encoding them (i.e. gene therapy).
CC The present sequence encodes a PSMA derived immunogenic peptide.
XX
SQ Sequence 27 BP; 8 A; 4 C; 5 G; 10 T; 0 other;

Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAATGATCAACTCATGTTTCTG 27
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DB 1 ATGATGAATGATCAACTCATGTTTCTG 27

RESULT 2
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ID ABK64577 standard; DNA; 442 BP.
XX
AC ABK64577;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #472.
XX
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX WPI; 2002-257476/30.
DR
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells
XX
PS Disclosure; Page 274; 444pp; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises

CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 442 BP; 127 A; 102 C; 71 G; 142 T; 0 other;

Query Match 100.0%; Score 27; DB 24; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAATGATCAACTCATGTTTCTG 27
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DB 385 ATGATGAATGATCAACTCATGTTTCTG 359

RESULT 3
ABV43616/c
ID ABV43616 standard; cDNA; 578 BP.
XX
AC ABV43616;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 43607.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8684; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds
(without alignments)
394.299 Million cell updates/sec

Title: US-09-821-734-16

Perfect score: 27

Sequence: 1 atgatgaatgatcaactcatgtttctg 27

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	70.4	678	4	US-09-134-001C-378
5	18	66.7	600	5	PCT-US93-10418-3
6	18	66.7	735	3	US-09-135-782-3
7	18	66.7	735	3	US-09-193-191-3
8	17.6	65.2	5577	1	US-08-326-117B-1
9	17.6	65.2	5577	3	US-08-982-129-1
10	17.6	65.2	5582	4	US-09-178-176B-1
11	17.6	65.2	5582	4	US-09-457-864-1
12	17.4	64.4	2423	2	US-08-365-486A-25
13	17.4	64.4	2423	4	US-08-880-342-25
14	17.4	64.4	3517	2	US-08-642-406A-20
15	17.4	64.4	3517	3	US-08-434-000A-1
16	17.4	64.4	3517	4	US-09-312-157-1
17	17.4	64.4	3517	4	US-09-199-534-20
18	17.4	64.4	3517	4	US-09-199-534-20
19	17.4	64.4	87350	3	US-08-781-891-79
20	17.4	64.4	87543	4	US-09-791-211-3
21	17	63.0	3016	4	US-09-221-017B-809
22	17	63.0	3134	4	US-09-668-680-1
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25	16.6	61.5	484	4	US-09-605-785-53
26	16.6	61.5	484	4	US-09-439-313-53
27	16.6	61.5	484	4	US-09-352-616A-53

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	30	16.6	61.5	1815	4	US-09-353-133-2	Sequence 2, Appli
	31	16.6	61.5	2001	1	US-08-674-168-24	Sequence 24, Appl
	32	16.6	61.5	2001	3	US-08-985-908-10	Sequence 10, Appl
	33	16.6	61.5	2001	3	US-08-852-730-23	Sequence 23, Appl
	34	16.6	61.5	2885	4	US-09-232-200-36	Sequence 36, Appl
	35	16.6	61.5	2885	4	US-09-232-200-56	Sequence 56, Appl
	36	16.6	61.5	2885	4	US-09-232-197-36	Sequence 36, Appl
	37	16.6	61.5	2885	4	US-09-232-197-56	Sequence 56, Appl
	38	16.6	61.5	2885	4	US-09-232-201-36	Sequence 36, Appl
	39	16.6	61.5	2885	4	US-09-232-201-56	Sequence 56, Appl
	40	16.4	60.7	977	4	US-08-976-259-18	Sequence 18, Appl
	41	16.4	60.7	1005	2	US-08-761-344-1	Sequence 1, Appli
	42	16.4	60.7	1239	4	US-08-887-534A-48	Sequence 48, Appl
	43	16.4	60.7	1239	4	US-08-887-534A-86	Sequence 86, Appl
	44	16.4	60.7	1569	2	US-08-761-344-3	Sequence 3, Appli
	45	16.4	60.7	1704	3	US-09-125-287-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-164-034B-1

GENERAL INFORMATION:

APPLICANT: Mincheff, Milcho S.

Loukinov, I. Dmitri

Zoubak, Serguei

TITLE OF INVENTION: Immunotherapy of Cancer Through Expression

of Truncated Tumor- or Tumor-Associated Antigen

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: William S. Ramsey,

Ramsey, Cook, Looper & Kurlander, LLC

STREET: 10420 Little Patuxent Parkway, Suite 250

CITY: Columbia

STATE: Maryland

COUNTRY: USA

ZIP: 21044

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: PC

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect 8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/164,034B

FILING DATE: 30-Sep-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ramsey, William S.

REGISTRATION NUMBER: 32,715

REFERENCE/DOCKET NUMBER: bril

TELECOMMUNICATION INFORMATION:

TELEPHONE: (410) 992-9660

TELEFAX: (410) 992-9540

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-164-034B-1

Query Match

Best Local Similarity 100.0%; Score 27; DB 4; Length 2133;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1861 ATGATGAATGATCAACTCATGTTTCTG 1887

RESULT 2

US-08-325-553-1

; Sequence 1, Application US/08325553

; Patent No. 5538866

; GENERAL INFORMATION:

; APPLICANT: Israeli, Ron S.

APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAATGATCAACTCATGTTTCTG 27
|||||
Db 2248 ATGATGAATGATCAACTCATGTTTCTG 2274

RESULT 3

US-08-394-152A-1
Sequence 1, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 2248 ATGATGAATGATCAACTCATGTTTCTG 2274

RESULT 4

US-09-134-001C-378
Sequence 378, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 378
LENGTH: 678
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-378

Query Match 70.4%; Score 19; DB 4; Length 678;
Best Local Similarity 81.5%; Pred. No. 9.4;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds
(without alignments)
703.471 Million cell updates/sec

Title: US-09-821-734-16
Perfect score: 27
Sequence: 1 atgatgaatgatcaactcatgtttctg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues 1186858

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	9	US-09-821-734-16
2	27	100.0	1037	10	US-09-925-300-86
3	27	100.0	2558	9	US-09-978-295A-617
4	27	100.0	2558	9	US-09-978-697-617
5	27	100.0	2558	9	US-09-978-192A-617
6	27	100.0	2558	9	US-09-999-832A-617
7	27	100.0	2558	9	US-09-978-189-617
8	27	100.0	2558	9	US-10-174-590-103
9	27	100.0	2558	9	US-10-176-758-103
10	27	100.0	2558	9	US-10-175-737-103
11	27	100.0	2558	9	US-10-173-706-103
12	27	100.0	2558	9	US-10-175-738-103
13	27	100.0	2558	9	US-10-175-752-103
14	27	100.0	2558	9	US-10-176-482-103
15	27	100.0	2558	9	US-10-176-757-103
16	27	100.0	2558	9	US-10-176-913-103
17	27	100.0	2558	9	US-10-180-552-103
18	27	100.0	2558	9	US-10-180-557-103
19	27	100.0	2558	9	US-10-173-700-103

20	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
24	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-743-103	Sequence 103, App
27	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
28	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
29	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
36	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
37	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
40	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
42	27	100.0	2558	9	US-10-174-586-103	Sequence 103, App
43	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
44	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-485-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-09-821-734-16
; Sequence 16, Application US/09821734
; Publication No. US20030027246A1
; GENERAL INFORMATION:
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Artur
; APPLICANT: Sia, Charles Dwo Yuan
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membran
; TITLE OF INVENTION: (PSMA) and Uses Thereof
; FILE REFERENCE: 11014-22
; CURRENT APPLICATION NUMBER: US/09/821,734
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,386
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CLP336

Query Match 100.0%; Score 27; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGATGATCAACTCATGTTTCTG 27
|||||
Db 1 ATGATGATGATCAACTCATGTTTCTG 27

RESULT 2
US-09-925-300-86
; Sequence 86, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 86
LENGTH: 1037
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-300-86

Query Match 100.0%; Score 27; DB 10; Length 1037;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAATGATCAACTCATGTTTCTG 27
|||||
Db 636 ATGATGAATGATCAACTCATGTTTCTG 662

RESULT 3
US-09-978-295A-617
Sequence 617, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:33:49 ; Search time 828.5 Seconds
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527.795 Million cell updates/sec

Title: US-09-821-734-16
Perfect score: 27
Sequence: 1 atgatgaatgatcaactcatgtttctg 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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		27:	em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	27	100.0	452	14	N64840	N64840 yz31h07.sl
C 5	27	100.0	471	9	AI356718	AI356718 qy17al2.x
C 6	27	100.0	474	9	AI474492	AI474492 th21d01.x

C	7	27	100.0	478	10	AW207840	AW207840 UI-H-BI2-
	8	27	100.0	492	14	N75691	N75691 yv29h07.r1
C	9	27	100.0	545	14	BQ027857	BQ027857 UI-H-CO0-
C	10	27	100.0	548	12	BF438644	BF438644 nab89b03.
C	11	27	100.0	618	9	AI766427	AI766427 wh49h09.x
C	12	27	100.0	690	9	AI672408	AI672408 ty64g12.x
C	13	27	100.0	720	12	BF940223	BF940223 nac70c04.
C	14	27	100.0	770	9	AI050871	AI050871 oy47b11.x
C	15	27	100.0	776	12	BG208080	BG208080 RST27570
C	16	27	100.0	797	12	BG202823	BG202823 RST22191
C	17	27	100.0	928	9	AL563970	AL563970 AL563970
C	18	22.2	82.2	420	9	AA879028	AA879028 nw87e05.s
C	19	22.2	82.2	421	10	AA879028	AA879028 nw87e05.s
C	20	22.2	82.2	462	9	AA897668	AA897668 oj78c06.s
C	21	22.2	82.2	575	13	BI538496	BI538496 433844.MA
C	22	22.2	82.2	659	13	BM537110	BM537110 ha78c03.g
C	23	22.2	82.2	745	13	BI183520	BI183520 UNL-P-FN-
C	24	20.6	76.3	569	12	BF334258	BF334258 RCI-CT024
C	25	20.6	76.3	801	12	BG185042	BG185042 RST3980.A
C	26	20.2	74.8	916	17	CNS03LW	AL249953 Tetraodon
C	27	19.8	73.3	499	9	AI545704	AI545704 fb75c06.y
C	28	19.6	72.6	424	17	AQ626285	AQ626285 CITBI-E1-
C	29	19.6	72.6	449	9	AI586754	AI586754 486060D07
C	30	19.6	72.6	489	9	AL730882	AL730882 AL730882
C	31	19.6	72.6	500	14	N51443	N51443 yzl7g02.sl
C	32	19.6	72.6	523	13	BM265401	BM265401 fw58h09.x
C	33	19.6	72.6	732	10	BE314435	BE314435 601145874
C	34	19.6	72.6	841	17	AZ677524	AZ677524 ENTLI35TR
C	35	19.6	72.6	891	17	AZ538793	AZ538793 ENTGS66TR
C	36	19.6	72.6	919	17	AZ668675	AZ668675 ENTI189TF
C	37	19.4	71.9	293	9	AU228501	AU228501 AU228501
C	38	19.4	71.9	626	17	BH116527	BH116527 RPCI-24-2
C	39	19.2	71.1	207	9	AA142314	AA142314 JMO0M045.
C	40	19.2	71.1	406	17	AQ761963	AQ761963 178P9CR.C
C	41	19.2	71.1	523	14	W96980	W96980 mf61a03.r1
C	42	19.2	71.1	526	9	AA050162	AA050162 mj17b03.r
C	43	19.2	71.1	531	14	W75581	W75581 me54f09.r1
C	44	19.2	71.1	908	17	CNS05BFM	AL329755 Tetraodon
C	45	19.2	71.1	2103	17	AG068108	AG068108 Pan trogl

ALIGNMENTS

RESULT 1	T29049	251 bp	mRNA	linear	EST 06-SEP-1995
LOCUS	EST66546	Human Prostate gland Homo sapiens	cdna 5'	end similar to	
DEFINITION	prostate-specific membrane antigen (HT:361), mRNA sequence.				
ACCESSION	T29049				
VERSION	T29049.1	GI:611147			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 251)				
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult ,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White ,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald ,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei ,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and				

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
JOURNAL Based Upon 83 Million Basepairs of cDNA Sequence
MEDLINE Nature 377, 3-174 (1995)
COMMENT 96026280
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.

FEATURES source

Location/Qualifiers
1. .251
/organism="Homo sapiens"
/db_xref="ATCC (inhost):105130"
/db_xref="taxon:9606"
/clone_lib="Human prostate gland"
/note="Organ: prostate gland"
BASE COUNT 80 a 37 c 36 g 97 t 1 others
ORIGIN

Query Match 100.0%; Score 27; DB 14; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAATGATCAACTCATGTTTCTG 27
|||||
Db 119 ATGATGAATGATCAACTCATGTTTCTG 145

RESULT 2
AW000926/c
LOCUS
DEFINITION
AW000926 426 bp mRNA linear EST 08-MAR-2000
wr90e01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494968 3',
similar to gb:M99487 PROSTATE-SPECIFIC MEMBRANE ANTIGEN (HUMAN);,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AW000926.1 GI:5847842
EST.
human.

REFERENCE
AUTHORS
TITLE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 523 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .426
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2494968"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;

FEATURES source

Location/Qualifiers
1. .426
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2494968"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo.
BASE COUNT 126 a 98 c 64 g 138 t
ORIGIN

Query Match 100.0%; Score 27; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAATGATCAACTCATGTTTCTG 27
|||||
Db 392 ATGATGAATGATCAACTCATGTTTCTG 366

RESULT 3
N48056/c
LOCUS
DEFINITION
N48056 442 bp mRNA linear EST 14-FEB-1996
yy99cl2.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA
clone IMAGE:281686 3' similar to gb:M99487 PROSTATE-SPECIFIC
MEMBRANE ANTIGEN (HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
N48056.1 GI:1189222
EST.
human.

REFERENCE
AUTHORS
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 442)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 284.
Location/Qualifiers
1. .442
/organism="Homo sapiens"
/db_xref="GDB:3900062"
/db_xref="taxon:9606"
/clone="IMAGE:281686"
/clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCATTTTCTTTTCTTTT 3']

TITLE
JOURNAL
COMMENT

Unpublished (1995)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 284.
Location/Qualifiers
1. .442
/organism="Homo sapiens"
/db_xref="GDB:3900062"
/db_xref="taxon:9606"
/clone="IMAGE:281686"
/clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCATTTTCTTTTCTTTT 3']

FEATURES source

Location/Qualifiers
1. .442
/organism="Homo sapiens"
/db_xref="GDB:3900062"
/db_xref="taxon:9606"
/clone="IMAGE:281686"
/clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCATTTTCTTTTCTTTT 3']